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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_ba1:
2: gb_ba2:
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336
1 CGCTGCATCTTTTT
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SCORE Match Length DB ID 80.6 24.0 119945 92 HSA218J18 80.6 24.0 162409 67 ACO22184 78.8 23.5 1846 93 HSNDPG 77.2 23.0 1872 93 HSCHRX 59.2 17.6 1769 94 MMNDP 59.2 17.6 1769 94 MMNDP 59.2 17.6 1769 94 MMNORRIE 41 12.2 115958 85 ACO04736 Human Chr

Result

C No

ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 HSA218J18/c LOCUS DEFINITION CESSION VERSION KEYWORDS SOURCE	0 0 9 34 0 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 119945)  Wray, P.  Direct Submission Submitted (26-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the	HSA21 Human Conta Splic seque AL034 AL034 HTG;	34.8 10.4 171445 61 ACO10136 ACO10136 Homo sapi   3 9.8 151036 65 ACO18471 ACO18471 Homo sapi   3 9.8 164036 65 ACO18471 ACO18471 Homo sapi   3 9.8 161536 67 ACO22064 ACO22064 Homo sapi   3 9.8 18161547 74 ACO63409 ACO73530 ACO6059 Homo sapi   3 9.8 18161547 74 ACO63409 ACO73530 Homo sapi   3 9.8 180606 74 ACO73530 ACO6059 Homo sapi   3 9.8 180606 74 ACO73530 ACO63409 ACO73530 Homo sapi   3 9.8 180606 74 ACO63409 ACO73530 Homo sapi   3 0.8 180606 74 ACO63408 ACO634728 Homo sapi   3 0.8 180606 74 ACO63773 ACO63775 ACO63775 Mus muscu   3 0.8 180490 74 ACO63120 ACO13416 Homo sapi   3 0.8 180490 74 ACO63120 ACO13416 Homo sapi   3 0.8 180490 74 ACO63733 ACO63732 Mus muscu   3 0.8 180490 74 ACO63733 ACO63732 Homo sapi   3 0.8 180490 74 ACO63733 ACO63732 Homo sapi   3 0.8 180490 74 ACO63733 ACO63732 Homo sapi   3 0.8 180490 74 ACO133185 ACO23185 Homo sapi   3 0.8 180490 74 ACO133185 ACO23185 Homo sapi   3 0.8 180490 74 ACO133185 ACO23185 Homo sapi   3 0.8 180490 74 ACO23185 ACO23185 Homo sapi   3 0.8 180490 74 ACO23185 ACO23185 Homo sapi   3 0.8 180490 74 ACO23131 ACO23131 Homo sapi   3 0.8 180490 74 ACO31333 ACO24610 Homo sapi   3 0.8 180490 74 ACO31335 ACO236410 Homo sapi   3 0.8 180490 74 ACO31353 ACO236410 Homo sapi   3 0.8 180490 74 ACO31353 ACO236410 Homo sapi   3 0.8 180490 74 ACO31353 ACO236410 Homo sapi   3 0.8 180490 74 ACO31365 ACO236455 Homo sapi   3 0.8 180490 74 ACO313

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FEATURES
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IMPORTANT: This sequence is not the entire insert of clone 218J18.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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/note="MLTID repeat: matches 72.
13498...13651
/note="L2 repeat: matches 2447...
14071...14210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MSTD 9797. .9923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MSTD repeat: matches 1. .394 of consensus"
9767. .9798
                                                                                                                                16904. .16998
/note="LIP repeat: matches 4891.
17144. .17247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 12651. .13006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 32. .245 of consensus"
11868. .12249
/note="Tigger3(Golem) repeat: matches 1. .3035 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="p11.3-11.4"
/clone="RP6-218J18"
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/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                            /note="MER74A repeat: matches 1..431 of consensus"
15386.16018
| note="11MB4 repeat: matches 5181.5827 of consensus"
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/note="28 copies 2
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                                                                                                                                                                                                    /note="AluSx repeat: matches 35.
                                                                                                                                                                                                                                          16519. .16720
note-"Alusg/x repeat: matches 100. .295 of consensus"
                                                                                                                                                                                                                                                                                     L5972. .16516
note="TLIP_repeat: matches 4397. .4940 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 2605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MLT1D repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER58A repeat: matches 42. .223 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MLT1H repeat: matches 391. .518 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"LTRIGA repeat: matches 92. .450 of consensu: complement(join(28998. .30248,38694. .39074,53526./gene-"NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24961
 /note="MIR repeat: matches 27. 36253. .36416
                                                                                                       /note="MER5A repeat: matches 9.
33816. .34022
                                                                                                                                                                                           /note="16 copies 2 mer ac
complement(33360. .33924)
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/gene="NDP"
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/gene="NDP"
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AA045724 AA670439 W61129 N59262 AA045724 AI129296 W61
N76731 R84741 H85821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="FLAM_A repeat: matches 1.
25646. .25750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 48. 20701. .20969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="LIMC4 repeat: matches 7788. .7954 of consensus"
20579. .20700
                                                                        34667.
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22317. .22579
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20970. .21069
                                      /note="L2 repeat: matches 2579. .2698 of consensus"
35507. .35714
                                                                                                                                                                                                                                                                                                                                                       /note="26 copies 2 mer aa 73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product=not_experimental
/protein_id=P(AA22258.1"
/db_xref="G1:3947697"
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25901. .26177
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25000. .25119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 17.
24827. .24928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER33 repeat: matches 62.
23269. .23575
                                                                                                                                                                              /gene="NDP"
                                                                                                                                                                                                                                              note="L2 repeat: matches
                                                                                                                                                                                                                                                                                note="FAM repeat: matches 1.
                                                                                                                                                                                                                                                                                                 'note="AluJo repeat: matches 1. .308 of consensus"
32205. .32377
                                                                                                                                                                                                                                                                                                                                                                      'note="MER5B repeat: matches 58. .178 of consensus"
30652. .30703
                                                                                                                                                                                                                                                                                                                                                                                                                         KALRLRCSGGMRLTATYRYILSCHCEECNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NDP"
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                                                                                     note="MIR repeat:
                                                                                                                                                          'note-"match: GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: proteins Q00604 P48744"
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                                                                     .34794
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                                                                                                                                                            AQ042323"
                                                                                       matches
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                                                                                                                                                                                                                                                                                  . 173
                                                                                                                                                                                                                                                                                                                                                     conserved"
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                                                                                         . 213
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                                                                                                                                                                                                                 conserved'
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                    . 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .281 of
                                                                                                                        .189 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .306 of consensus"
                                                                                                                                                                                                                                                . 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .133 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .324 of consensus
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                    of consensus"
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                                                                                                                                                                                                                                                                                            TITLE
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Best Local
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146; Conserv
             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, C., Barna, N., Beckerly, R., Beda, F., Boukhyalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Mann, L., Karatas, A., Klein, J., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Fortest, C., Gardyna, S., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Fortest, C., Gardyna, S., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Fortest, C., Fortest, G., Kann, L., Karatas, A., Klein, J., Fortest, C., Fortest,
                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Carl (bases 1 to 162409)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 4 clone SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 4, clone RP11-52G4
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56812. .57069
/note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="15 copies 2 mer aa 87% 48315, .48514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: STS AF020217" 51372. .51487
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/note="L1M4b repeat: matches 154.
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53680. .53741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluJb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162409 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.6; DB 92;
Pred. No. 1.6e-15;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
Levine, R.,
                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP11-52G4 map 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 92;
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Liu,G.,
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Locke, K.,
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Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

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FEATURES
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                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPheeters,R., MeIdrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
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Insert size: 161309; sum-of-contigs
Quality coverage: 3.7 in Q20 bases;
Quality coverage: 4.3 in Q20 bases;
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Center clone name: 52_G_4
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27971 28070: gap of 100 bp
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/clone="RP11-52G4"
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/chromosome="4"
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12552: contig of 2456 bp in length
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Breakefield, X.O.,
                                Submitted (28-APR-1992) Z. Lab/Dept of Biochemistry, (2 (bases 1 to 1846)
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1846)
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                                                                                             Chen
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28071. .36727
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Hendriks,R.W., Joblir
d,X.O., Sims,K.B. and
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              Jobling, M.A.,
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             Berger, W.
Direct Su
                                                                                                                                                                                                                                 H.sapiens DNA for ORF1
                                                                                                 1 (bases 1 to 1872)
Berger, W., Meindl, A., van de Pol, T.J., Cremers, F.P., Ropers, H.H., Doerner, C., Monaco, A., Bergen, A.A., Lebo, R., Warburg, M. et, al. Isolation of a candidate gene for Norrie disease by positional
Submitted (08-APR-1992) W. Berger, University Hospital Nijmegen,
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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vDsishplykcsskmvllarceghcsQasrseplvsfsTvlkQpfrssChCcrpQTSk
LkalrlrcsggmrltatyryIlsChCeecns"
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85. .92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/chromosome="Xp11.23"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"SWISS-PROT:Q00604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA46713.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="retina"
/clone_lib="fetal retina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78.8; DB 93; Pred. No. 5.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
Submitted (05-JAN-1995) Z. Chen, Molecular Neurogenetics Lab, Massachusetts General Hospital-East, Building 149, 13th Stree Charlestown, MA 02129, USA Location/Qualifiers
                                                                          Chen, Z.
Direct Submission
                                                                                                                                                                                           Characterization and mapping of the
                                                                                                                                                                                                                 Chen, Z.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dept of Human Genetics, Geert Grooteplein Nijmegen, THE NETHERLANDS
                                                                                                                                                                                                                                   Battinelli, E.M., Boyd, Y., Craig, I.W.,
                                                                                                                                                                                                                                                      Mammalia; Eutheria;
1 (bases 1 to 1769)
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                      NDP gene;
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                                                                                                                                                                                                                                                                                                                                      house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                             .musculus NDP gene.
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ISFGSFSDSGIFPLGSQCCLGFQQFSISGKKWALIHKRVRLSVFGARWGRIYFGK"
425 c 409 g 517 t
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/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDSISHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
                                                                                                                                                                                                                                                                                                                                                      GI:854318
Norrie disease locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA46640.1"
/db_xref="GI:1335017"
/translation="BHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKALRLRCSGGMRLTATYRYILSCHCEECNS"
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/db_xref="GI:29947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1769 bp
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Pred. No. 1.9e-14;
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                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 93;
                                                                                                                                                                                                 mouse
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Submitted (17-OCT-1995) W. Berger, No. 10 Innestrasse 73, D-14195 Berlin, FRG
                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1774)

Berger, W., van de Pol, D., Bachner, D., Oerlemans, F., Winkens, H., Hameister, H., Wieringa, B., Hendriks, W. and Ropers, H.H.
                                                                                                                                                                                                                                Hum. Mol. Genet. 5 (1), 51-59 (1996) 96381426
                                                                                                                                                                                                                                                                   Hameister,H., Wieringa,B., Hendriks,W. ar
An animal model for Norrie disease (ND):
                                                                                                                                                                                                                                                                                                                                                                                           X92397.1 GI:1177544
ND gene; Norrie disease locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MMNORRIE 1774 by
M.musculus mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                               Berger,W
                                                                                                                                                                                                                                                             mouse
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                                                                                                                                                                                                                                                      ND gene
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                                                          /db_xref="taxon:10090"
/chromosome="X"
                                                                                     /organism="Mus musculus"
/strain="C57/b16"
/number=1
           /tissue_type="brain"
L. .225
                                         /dev_stage="19 weeks"
                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-:PROT:P48744"
//tanslation="mrnhyLAASISMLSLLAINGDTDSKTDSSFLMDSQRCMRHHYVD
SISHPLYKCSSKMYLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSKLK
ALRLRCSGGMRLTATYRYILSCHCEECSS"
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429. .8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NDP"
429. .824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA58725.1"
/db_xref="GI:854319"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="embryonic stem cells"
/cell_type="ES cells"
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/chromosome="X"
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/strain="L129"
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87.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        norrie disease
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Pred. No. 1.6e-08;
0; Mismatches 9
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                                                                                                                                                          MPI fuer Molekulare Genetik,
                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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RS Birren, B., Linton, L., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

RS Birren, B., Linton, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

RS Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hilme, W., Illev, I., Johnson, R.,

Jones, C., Karatas, A., LaRocque, K., Lamaczes, R., Landers, T.,

Lehoczky, J., Levine, R., Liu, G., MacLean, C., McKernan, K.,

Marquis, N., Matthews, C., McCarthy, M., McBwan, P., McKernan, K.,

McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C., H.,

O'Connor, T., O'Donnell, P., O'Weil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,

Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,

Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Travers, M., Travis, N., Trajalio, J., Vassiliev, H., Viel, R., Vo, A.,

Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,

Zembek, L., Zimmer, A. and Zody, M.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-300E4
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/translation="MRNHVLAASISMLSLLAIMGDTDSKTDSSFLMDSQRCMRHHYVD
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         Zimmer, A. and Zody, M.
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/protein_id="CAA63134.1"
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All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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49371:

71: gap of 50018: contig

100 bp of 647 bp

Stimson, S., Syed, M. and Ward, T

Basit,M.,

Gotway, G.,

Harry Hines

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                     3 (bases 1 to 115958)

Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M., Buettner,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J., English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G. Grant,O., Hahner,L., Harris,J., Lewis,E., Loo,H., Loo,K.N.,
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EVans.G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M., Bumetner, J., Bumeister, R., Card, P., deSailboat, C., Dunn, J., English, C., Ethridge, S., Garner, H.R., Gee, V., Gordon, M., Gotw. Grant, O., Hahner, L., Harris, J., Lewis, E., Loo, H., Loo, K.N., McFarland, J., Schultz, R., Newton, J., Osborne-Lawrence, S., Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T.
                                                                                                                                                              Submitted (23-MAY-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans, G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M. Buettner, J., Bumeister, R., Card, P., deSailboat, F., Dunn, J., English, C., Ethridge, S., Garner, H.R., Gee, V., Gordon, M., Gol Grant, O., Hahner, L., Harris, J., Lewis, E., Loo, H., Loo, K.N., Major, T., McFarland, J., Newton, J., Osborne-Lawrence, S., Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T.
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1 (bases 1 to 115958)
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Human Chromosome 11p14.3 PAC clone pDJ1082L12 containing KNCN1 and
MYOD, complete sequence.
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50840 50939: gap of 100 bp
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51665 51764: gap of 100 bp
51765 52477: contig of 713 bp in length
52478 52577: gap of 100 bp
52578 53281: contig of 704 bp in length
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55782: gap of 100 bp
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IMPORTANT: This submission contains the entire insert of clone pDJ1082L12. pDJ1082L12 comes from a PAC library constructed at the Roswell Park Cancer Institute by the pieter de Jong group. This clone has been finished according to strict quality criteria and attempts have been made to resolve all base calling problems such as compressions and repetitive elements. The expected Phred/Phrap calculated errors/10kb is 0.39. In addition, this sequence has been finished such that 99.9% of consensus base calls consist of either double-stranded coverage or 2 types of labeling chemistry o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-UII-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA
On Jul 1, 1998 this sequence version replaced 91:3152625.
NOTE: Extent of pDJ1082L12 overlap with mapped clones; SP6 PAC cloning end: 1. 8775, pDJ59ml8; T7 PAC cloning end: 45252. .115958.
6-109h6. Further information regarding the map of this region or annotation of pDJ1082L12 can be found at http://gestec.swmed.edu/chromoso2.htm.
CHROMSOMAL LOCUS: This PAC clone comes from the Usher syndrome region (USH1C) mapped between STSs markers D11S1310 and 1115A14.
MARKER CONFIRMATION: STSS/ESTS sequence confirmed; D11S4130, KNCN1,
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                                                                                                                                                                                                                                                                                                  173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232
                                                                                                                                                                                                                                    233 TGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTCCTTGGN 292
                                                                                                                                                                                      293 CAGNAGNAANGGANTTGGNCC 313
                                                                                                                                                                                                                      TGATGGAACGTCCGCCTGCCAGGGGAGAGGGAGGGAGGGCCGCTGACATCAGGCCTTGGT 41455
                                              ACO10136 171453 bp DNA HTG . 22-MAR-20 Homo sapiens chromosome UNK clone RP11-129D2, WORKING DRAFT SEQUENCE, 2 unordered pieces.
ACO10136.7 GI:13431097
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                   AC010136
                                                                                                                                                                                                                                                                                                                                               Conservative
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86387.
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complement(112629. .112992)
/rpt_family="L1"
29554 c 29450 g 28568 t
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/rpt_family="L1"
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/rpt_family="Alu"
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complement(107302. .107596)
/rpt_family="Alu"
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/rpt_family="L1"
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/rpt_family="MLT1"
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94274. .94419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(88437.
/rpt_family="MIR"
complement(90686.
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84727. .85172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu" complement(82106. /rpt_family="Alu"
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111412. .111792
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109188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(106369. .106641)
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105673. .105884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105586.
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/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y-"MIR"
                                                                                                                                                                                                                                                                                                                                          Score 41; DB 85; Length 115958; Pred. No. 0.019; 0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .95617)
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                                                                             22-MAR-2001
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JOURNAL
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AUTHORS
TITLE
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AUTHORS
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В
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ORIGIN
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ORGANISM
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                                                                               Matches
                                                                                                Query Match
Best Local
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                    202 CCCCGNNTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAA 261
                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer ET; 52% of reads chemistry: Dye-terminator Big Dye; 48% of reads Assembly program: Phrap; version 0.990319 consensus quality: 169816 bases at least Q40 consensus quality: 170375 bases at least Q30 consensus quality: 170797 bases at least Q20 Insert size: 198000; agarose-fp Insert size: 171353; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Mar 22, 2001 this sequence version replaced di-11990739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 7.08 in Q20 bases; agarose-fp Quality coverage: 7.13 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 58%
Sequencing vector: plasmid; 42%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 171453)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                h 10.4%;
Similarity 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Genome Center -----
                                                                                                                                                                                                       38981
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32329 32428: gap of unknown length
32429 171453: contig of 139025 bp in length
                                                                               Conservative
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                                                                                                                                                                                                                                                             vector_side:left"
32429 .171453
/note="assembly_name:Contig8
                                                                                                                                                                                                                      vector_side:right"
                                                                                                                                                                                                                                              clone_end:SP6
                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig7
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="UNK"
/clone="RP11-129D2"
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                                                                                                                                                                                                     41426 c 46891 g
                                                                                                                                                                                                                                                                                                                                                                        .32328
                                                                             Score 34.8; DB 61;
Pred. No. 2.2;
0; Mismatches 54;
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                                                                                                                                                                                                         100 others
                                                                                                                   Length 171453;
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RESULT 1
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RESULT 11
AC018471/c
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                                                                               2768 GACAGCTTGACAGCTGGTCAAGACGGTCAC 2797
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                                                                                                                    62 GACAGCTCGTNTCATGATCGACTCGGACCC 91
                                                                                                                                                                               GTTTCATGTTCTTGTACACTTCCCCTCTGGGATCAGGTGAGGGGTCCAGACAGCTGACCA 2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain DNA Res. 6 (5), 329-336 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohara, O., Nagase, T. and Kikuno, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SK plus clone:hg03443a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB033016.1 GI:6330337
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                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3510)
                                                                                                                                                                                                                                                                                                                                                              693
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="KIAA1190"
<1. .527
                                                                                                                                                                                                                                                                                                                                                                                 PTTASPGGRMNANN"
                                                                                                                                                                                                                                                                                                                                                                                                    KAHKEKCFRVSHTLAGDGVPAAPGLPPTQPQAHALPLLPGLPQTLPPPPHLPPPPPLF
                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="kpfrcencnereqykyqlrshms1h1ghkqfmcqwcgkdfnmkqyfdehmkthtgekpy1ce1cgksftsrpnmkrrthtgekpypcdvcgqrfrfsnml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="KIAA1190 protein"
/protein_id="BAA86504.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Start codon is not identified."
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="KIAA1190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="hg03443a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA86504
/db_xref="GI:6330338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="brain"
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for KIAA1190 protein,
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                                                                                                                                                                                                                                           Mismatches
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Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F.,
Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Davy-Carroll, L., Dubin, K.J., Earnhart, C., Edgar, D., Edwards, G.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Lewis, L., Li, J., Li, K., Karls, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liua, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, N.,
Nguyen, A., Nguyen, N., Nickerson, E., Nuchela, N.,
Nguyen, A., Svatey, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Stone, H., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Plomas, S., Warf Moore, S., Warren, R., Washington, C.,
Nand C., Wu, C., Wu, Y., F., Zhou, J., Villalon, D., Vinson, R.,
Wall, R., Washington, C.,
Wall, R., Wan, S., Wall, R., Shooshtari, N.,
Nogu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2000 this sequence version replaced gi:9719644.
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Homo sapiens chromosome
18 unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Pr
1 (bases 1 to 164036)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chemistry: Dye-primer Bodipy: 46% of reads Chemistry: Dye-terminator Big Dye: 54% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 150896 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Center code: BCM
                                                                                                                                                                            Center clone name: RP11-132K4
Summary Statistics
                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                               Sequencing vector: M13;
                                                                                                                                                                                                                                                      Center project name: HMVD
                                                                                                                                                                                                                                                                                   Project Information
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Jb 112240 GACAGCTTGACAGCTGGTCAAGACGGTCAC 112211
                                                                                                                                                                       BASE COUNT
ORIGIN
                                                   Db 112300 GTTTCATGTTCTTGTACACTTCCCCTCTGGGATCAGGTGAGGGGTCCAGACAGCTGACCA 112241
                                                                                                                                                                                                                                                                     SATURES
                                                                                                       Matches
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Best Local
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                                                                                                                    Local
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               GACAGCTCGTNTCATGATCGACTCGGACCC 91
                                                                           Similarity
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NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                       43123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 157400 bases at least Q30 Consensus quality: 160584 bases at least Q30 Estimated Insert size: 160109; sum-of-contigs estimation Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                   /clone="RP11-132K4"
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                                                                                                                                                                                                                                                                  Location,
                                                                                                                  9.8%;
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                                                                                                                  Score 33; DB 65; Length 164036; Pred. No. 8.5;
                                                                                                       Mismatches
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of 4337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6778492. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., TheodriftellA., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-296G21 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choepel,Y.,
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HTG; HTGS_PHASE1; HTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169523 bases at least Q40
Consensus quality: 169523 bases at least Q30
Consensus quality: 177188 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 178259; sum-of-contigs
Quality coverage: 5.2 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contig
                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                       1138 1237: gap
1238 2271:
1238 2271: contig of 1034 bp
2272 2371: gap of 100 bp
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                                                                              1137: contig of 1137 bp in length
7: gap of 100 bp
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Primates;
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RP11-296G21 map 15, WORKING DRAFT
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Wu,X., Wyman,D., Ye,W.J.
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15744 17047: contig of 1304 bp
17048 17147: gap of 100 bp
17148 18830: contig of 1683 bp
18831 18930: gap of 100 bp
18931 20799: contig of 1869 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55406 55505; gap of 100 bp
55506 71682; contig of 16177 bp in length
71683 71782; gap of 100 bp
71783 97873; contig of 26091 bp in length
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20900 25005: con
25006 25105: gap of
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6104 7238: contin of
7239 7230
                                                                                     /note="assembly_fragment" 11752. .13621
/note="assembly_fragment"
17148. .18830
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19 7338: gap of 100
9 8789: contig of 1
0 8880.
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4932. .6003
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2372. .3377
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15744. .17047
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4831:
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13722. .15643
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1238. .2271
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                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                               clone="RP11-296G21"
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11751: gap of 100 bp
13621: contig of 1870 bp in length
13721: gap of
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10365: cor
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31884: contig of 6779 bp in length
384: gap of 100 bp
44283: contig of 12299 bp in length
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15643: contig of 1922 b
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contig of 1476 bp
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of 1135 bp
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Direct Submission
Submitted (30-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                 Worley, K.C.
Direct Submission
                                                                                                                                                            Submitted (26-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,J., Chen,Z., Culpepper,P., Ding,Y., Dugan,S.P., Durbin,K.J., Forcum,J., Ganesh,R.P., Garcia,C., Garcia,D.K., Gorrell,H., Gorrell,L.L., Hernandez,J., Jackson,L.E., Kondejewski,N., Leal,B., Lichtarge,O., Liu,W., Logan,O., Lu,J., Martinez,C., Moore,S., Moorish,T., Ngyuen,N., Oswal,G., Panpell,L.R., Parish,B.J., Derger, L. Backid, N.D., Diroc, C. M., Cocker, C. Backer, C
                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                      Unpublished
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Homo sapiens PAC RPCI4-613B23 (Roswell Park Cancer
PAC Library) complete sequence.
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97974. .127625
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25106. .31884
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127726. .180359
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20900. .25005
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.M., Scherer,S.E., Shen,H.,
liamson,A.L., Worley,K., Zhc
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TITLE
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-APR-1999) Human Genome Sequencing Center, Depois Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA on Mar 30, 1999 this sequence version replaced gi:4263627. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                     Position
28864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rates than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation
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Phrap values in estimate:
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RESULT 14
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 161547)

CE 1 (bases 1 to 161547)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowley, R., Briange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhke, C., Cartor, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, S., Chevel, C., Chen, C
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AC073530
AC073530.17 GI:13162369
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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HOMO sapiens chromosome 12 clone RP11-123010, WORKING DRAFT
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/mpt_family="LIM4"
complement(10753. .11023)
/mpt_family="Aludo"
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/rpt_family="(CA)n"
10424. .10497
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8464. .9146
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/rpt_family="(TAAA)n"
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/rpt_family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 28, 2001 this sequence version replaced gi:13123810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
Direct Submission
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Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 15% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Assembly program: Phrap; version 0, 990329
Consensus quality: 160458 bases at least Q30
Consensus quality: 161972 bases at least Q30
Consensus quality: 161972 bases at least Q30
Consensus quality: 163257 bases at least Q30
Estimated insert size: 157486; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: RP11-123010
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COMMENT

REFERENCE TITLE JOURNAL AUTHORS JOURNAL TITLE

BASE COUNT source arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence (see http://www.hgsc.bcm.tmc.edu/doos/Genbank\_draft\_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is NOTE: Estimated insert size may differ from sequence length be preserved as soon as it is available and the accession number will 156391 156491 157493 157593 158939 159039 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="12" /clone="RP11-123010" Location/Qualifiers
1. .161547 156390: contig of 156390 bp in length 156490: gap of unknown length 157492: contig of 1002 bp in length 157592: gap of unknown length 158938: contig of 1346 bp in length 159038: gap of unknown length 31335 g contig of 1222 gap of unknown contig of 1187 49855 t bp in length bp in length 415 others length.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC069409.7 GI:9966586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sep 5, 2000 this sequence version replaced gi:8844019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 177765)
                                Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 6% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 156950 bases at least 040
Consensus quality: 164968 bases at least 020
Consensus quality: 170263 bases at least 020
Estimated insert size: 169417; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 177765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: RP11-308L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
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Pred. No. 9.8;
3.2x in Q20 bases; sum-of-contigs estimation
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Query Match Best Local S Matches 52

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Indels

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Gaps

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Score 32.8; Di Pred. No. 9.9; 0; Mismatches

DB 74; Length 177765;

9.8%;

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BASE COUNT
ORIGIN
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved
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/db_xref="taxon:9606"
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                       Lone="RP11-308L22"
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Search completed: August 24, 2001, 03:54:00 Job time: 4216 sec

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Database
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

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2834	7566	2302	1389	1322	49136	536165	534720	34263	34203	10732	3287	1399	4089	3621	3416	3416	849	7560	7346	7286	6744	2773	2921	49999	14784	2602	1246	1169	1169	1169	1166	1160	15914
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AAN90394	AN70307	AAX86274	AAF67781	AAC33434	AAA27475	AAV30459	AAV30458	AAF74547	AAF74546	AAA10594	AAC98900	AAQ11843	AAZ36693	AAV17800	AAV40859	AAT30373	AAC49585	AAC83437	AAX77924	AAT14547	AAZ38125	AAZ22704	AAA30884	AAZ23901	AAA64141	AAT93309	AAT93286	AAT93284	AAT93283	AAT93282	AAT93285	AAT93294	AAF57269
Genomic DNA of hum	of hims	DNA encoding a him	Corynebacterium ql	Arabidopsis thalia	NIDDM1 region incl	Rhizobium species	Rhizobium species	Penicillium citrin	Penicillium citrin	Gene encoding a su	Human pancreatic c	Human lactoperoxid	Nucleotide sequenc	Human related adhe	Human PYK-2 protei	Probin tyrosine ki	Arabidopsis thalia	Human tenascin-C.	Human tenascin cDN	Cytotactin gene.	Human FATP genomic	Pseudomonas fluore	Mouse GFAT II codi		Nucleotide sequenc		mottle	mottle	mottle		Tomato mottle viru	le	Mouse RetL5 genomi

## ALIGNMENTS

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RESULT
                                                                                                                          AAC76650
                                    08-FEB-2001
                                                                                                        AAC76650 standard; cDNA; 4217
Human ORFX ORF2205 polynucleotide sequence SEQ ID NO:4409
                                                                                                                                         ш
                                  (first entry)
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immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic, gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; hone damaen as cartillary and haemoglobinuria; burn; wound; Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; thrombosis; bone damage; cartilage damage; antiinflammatory disease; coagulation; contraceptive; hypertension;

Homo sapiens.

WO200058473-A2

05-OCT-2000.

31-MAR-2000; 2000WO-US08621

31-MAR-1999; 99US-0127607

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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                         Homo sapiens
                                                                                                    excitatory amino acid
                                                                                                                           Human EAA3c excitatory amino acid receptor cDNA.
                                                                                                                                                                 22-MAR-1995
                                                                                                                                                                                                AAQ81157;
                                                                                                                                                                                                                         AAQ81157 standard;
                                                                                                                                                                                                                                                                                                       3459
                                                                                                                                                                                                                                                                                                                                                3399 gtttcatgttcttgtacacttcccctctgggatcaggtgaggggtccagacagctgacca 3458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4217 BP; 888 A; 1243 C; 1230 G; 856 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                                                                                                                             62 GACAGCTCGTNTCATGATCGACTCGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                   gacagcttgacagctggtcaagacggtcac 3488
                                                                                     receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 3600-3603; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                              (first entry)
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99US-0127728.
2000US-0540763.
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            Location/Qualifiers
418..3015
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                                                                                               receptor; human EAA3 receptor;
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Pred. No. 0.49;
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Best Local;
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                            Arabidopsis thaliana DNA fragment SEQ ID NO:
        Hybridisation
                                                            17-OCT-2000
                                                                                      AAC36410;
                                                                                                             AAC36410 standard; DNA; 1147 BP
                                                                                                                                                                              2965 TATTCTTCCGTGATTTGTATATGAATTCTCCAATAGC
                                                                                                                                                                                                                                          3025
                                                                                                                                                                                                                                                                                                                                                                                                                                               EAA3d (AAR63068-R63070) occur naturally in human brain. They are all members of the EAA3 receptor family, having extracellular N- and C-termini and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
                                                                                                                                                                                               176 GAGTCTTCTGTGAGACCTATCTGAATCCCCGUNNTGGC
                                                                                                                                                                                                                                                         116 ATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGTGG 175
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                               N.B. The cDNA and corresp. amino acid sequences for EAA3b, 3c and 3d do not appear in full in the specification; the sequences have been compiled by combining sequences in Figures 1 and 4 according to the description given in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The human EAA3a receptor (AAR60112) and its variants EAA3b, EAA3c and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1 and Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide encoding a human excitatory amino acid 3 receptor or fragment - used to assay test ligands for their interaction with a human CBS receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KAMB/) KAMBOJ R.
(ELLI/) ELLIOT C E.
(NUTT/) NUTT S L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1994-255829/32
                                                                                                                                                                                                                                                                                             Similarity 54; Conser
                                                                                                                                                                                                                                                                                                                                                         3067 BP; 804 A; 747 C;
                                                                                                                                                                                                                                                                                          Conservative
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                                                         (first entry)
       assay;
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508..3012
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/product= EAA3c_receptor
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genetic mapping; gene expression control;
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55.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "encodes a truncated version of EAA3a in which 40 amino acids have been eliminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the C-terminus and in which the last 11 amino acids differ from those in the corresponding region of EAA3a"
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Pred. No. 1.7;
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990S-0139750. 990S-0139763. 990S-0139817. 990S-0139899. 990S-0140353.																										99US-0129845. 99US-0130077.	99US-0128714.	99US-0127462.	99US-0126785.	9119	900	99US-0121825.	2000EP-0301439.			•	thaliana.	c pathway; promoter; n
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07-SEP-1999; 10-SEP-1999; 13-SEP-1999;

16-SEP-1999 15-SEP-1999

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

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RESULT 4
AAC40084/c
ID AAC40084 standard; DNA; 1626 BP.
XX
AC AAC40084;
XX
DT 17-OCT-2000 (first entry)
XX
AC Arabidopsis thaliana DNA fragment
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atches 72; Conserv
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                                                                                                                                                                                                                                                                                         210 GGCCCTGAGNTTCCAGAGGGNCCTGGTCG 238
                                                                                                                                                                                                                                                                                                                                      318 CTAGCTACTCCATGGCATACGACTCCGTGTCTAACCCGCGACCGAGCAGCAGTCTCCACGT
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48.3%;
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                                                   NO:
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Tomato hsp80 genomic clone Ghsp-4(locus A).
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l Similarity 48.3%;
72; Conservative
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/note= "Exon 1"
2264..3259
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/note= "Intron 2"
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                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA constructs - comprising tomato heat shock protein non-coding region and gene region of interest, useful for producing transgenic plants with modified phenotype(s)
                                                    315 taaaaataattgagcttgtttgttgttagtacatgattc
                                                                                                                                                                                                                                                                                                                                                         the level observed in meristematic tissue.
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                                                                                            164 GAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATC 202
                                                                                                                              255 tgaggccaagctatctttaaaggtattgggtcacccgtatgtccaattgcatatgagaag
                                                                                                                                                                      104 TGAGGCACCACTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAG
6
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Pred. No. 4.1;
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AAX20446
19-AUG-1997;
30-JUL-1997;
30-JUL-1997;
                                                          29-JUL-1998;
                                                                                                                                                                cognitive disorder; schizophrenia; prostate; obesity; osteoclosteoporosis; arthritis; testis; lung; thyroiditis; thyroid; endocrine; metabolism; regulation; malabsorption; gastritis;
                                                                                                                                                                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                 WO9906423-A1
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          AAX20446;
                                                                                                                                                                                                                                                                                                Human secreted protein gene 35.
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 97US-0056730.
97US-0054209.
97US-0054211.
                                                        98WO-US15949
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                                                                                                                                                                                                                                                                                                                                               This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX20403) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 83 novel genes and their fragments (nucleic acid sequences: AAX20412-X20499; amino acid sequences AAX00258-Y00377) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in the new polynucleotides.
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18-AUG-1997;
18-AUG-1997;
19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
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30-JUL-1997;
30-JUL-1997;
                         02-FEB-2001
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P-PSDB; AAY00292.
                                                  AAA62025;
                                                                           AAA62025 standard; DNA;
                                                                                                                                                                                                                                                                                                               Sequence 965
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30-JUL-1997;
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PA, Rosen
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97US-0056554.
97US-0056561.
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97US-0055972.
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97US-0054217.
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97US-0054213.
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97US-0056729
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97US-0054236.
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channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoissis activity, tissue growth activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                            activin/inhibin activity, chemotactic/chemokinetic activity, haemostate and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                        cells. Membrane proteins have important roles as signal receptors, ion
                                                                                                                                                                                                                                                                                                                                                                                                            Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 303; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hemostatic, thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGA )
(PROT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-387753/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGAMI CHEM RES PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12142.
   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura T;
cancer via gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
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99JP-0119299
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98JP-0364315
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                                                                                                                                         haemostatic
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RESULT
AAC93406
ID AAC9
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                                                                                      Вb
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                                                                                                                                  Query Match
Best Local
                                                                                                                         Matches
         AAC93406 standard; cDNA; 1278
                                                                     233
                                                                                      974
                                                                                                                                 Local
                          8
                                                                                                TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232
                                                                      TGGTCGTCCCATCGCCTAGCAGGGTTC
                                                                                     tggtgggcacctcggcgggggtggtcc
                                                                                                                          50;
                                                                                                                                  Similarity
                                                                                                                          Conservative
                                                                                                                                  9.0%;
57.5%;
                                                                                                                         Score 30.2; E
Pred. No. 2.5;
0; Mismatches
                                                                                                                          0
         ВP
                                                    1060
                                                                      259
                                                                                                                                  5.
                                                                                                                                            BB
                                                                                                                          37;
                                                                                                                                            21;
                                                                                                                                          Length
                                                                                                                                            1275;
                                                                                                                          0
                                                                                                                          Gaps
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Sequence 1275

BP;

162

P

417 C;

406 G;

290

Ή,,

0 other;

0;

Hydrophobic domain protein cDNA HP10636 isolated from HT-1080 cells

26-FEB-2001 AAC93406;

(first entry)

protein

gene

43

SEQ

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NO:53

Q 밁

В

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CC invention. Human secreted proteins have activities based on the tissues CC and cells the genes are expressed in. Examples of activities include: CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative; CC existatic; cardiant; vasotropic; cerebroprotective; noctropic; CC neuroprotective; antibacterial; virucide; fungicide; and ophythalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a disorders, cerebrovascular disorders, angiogenesis, nervous system CC disorders, cerebrovascular disorders, angiogenesis, nervous system CC disorders. The polypeptides can also be used to aid wound healing and cc epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                           AAB51722 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polynucleotide sequences given in AAC93364 to AAC93412 encode thuman secreted proteins given in AAB51620 to AAB51668. AAB51669 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1999; 99US-0128702
20-JAN-2000; 2000US-0177049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antipacterial; virucid; fungicide; ophthalmological; gene therapy; autoimmune disease; infect hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2000; 2000WO-US09069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2000
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                                                        or decrease storage represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540pp; English
                                                 be used as a food additive or preservative storage capabilities. AAC93355 to AAC93363 a quences which are used in the exemplificatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komatsoulis
                                                   the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virucide;
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173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232

Matches

Loca1

Similarity

57

.58;

Score 30.2; Pred. No. 2

Conservative

0;

Pred. No. 2.5; ); Mismatches

37;

Indels Length

0,

Gaps

0;

Query Match

Sequence

1712

ВP;

246 A;

552 C;

538

G;

376 T;

0

Score

30.2;

DB 21; Sequence

1278

ВP;

259

Ą,

355

С;

379

G;

278

T; 7 other;

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RESULT
AAA62035
                                                                                                                                                         protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1998;
16-MAR-1999;
27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                               Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence
                                                                                                       activity, haematopoiesis activity, tissue growth activity, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various
                       and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                 channels and transporters. The present sequence is the coding sequence that the coding sequence is the coding sequence that the coding sequence is the coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAGA )
(PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biophylaxis; signal receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; membrane protein; hydrophobic doma
proliferation control; differentiation induction; material
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrophobic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12142.
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PROTEGENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                       Page 321-324; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain protein cDNA HP10636 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99JP-0119299
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This sequence encodes human G-protein coupled receptor protein (GCRP) The GCRP polypeptides, polynucleotides, antibodies, antagonists and agonists may be administered to human patients for the diagnosis, treatment and prevention of nervous system disorders (e.g. epilepsy, stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory disorders, complications of cancer, hemadialysis and extracorporeal circulation, and cell proliferative disorders. They are also used to treat or prevent disorders associated with decreased or increased expression or activity of GCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; antiasthmatic; antianemic; antiarteriosclerotic;
antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory;
antigout; thyromimetic; haemostatic; virucide; hepatotropic; osteopathic;
                                                                                                                                                                                                                                                                                Novel human G-protein coupled receptor proteins used in treatment and prevention of nervous system disorders, autoimmune/inflammatory disorders, and cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor protein 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1998;
06-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCRP-8; G protein-coupled receptor protein; antipsoriatic; antirheumatic
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                                                                                                                                                                                                                     Claim 9; Page 79-80; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1 hes 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0167219.
98US-0172211.
99US-0133585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal ·P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Baughn
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandman
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Azimzai
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                                                                                                                                                                                                                                                                                  cell proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽,
                                                                                                                                                                                                                                                                                                                          the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley
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                                                    They are
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Query Match

.08;

Score

30.2;

DB

21;

Length 2171;

Ъ Qy

38

167 GAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGA 226

gagtattcccactttcctgtgcggtgcagcagtatgcctgggggaagatgggttccaaca

Matches

1 Similarity 76; Conserv

Conservative

0;

90; 21;

Indels

Gaps

0

8.98; 45.88;

Score 29.8; DE Pred. No. 2.2; 0; Mismatches

DВ

Length

441; 0

Query Match Best Local

Sequence

2171

ВP;

297

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721

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707

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446

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0 other;

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AAC02302
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                                    derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1661
                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                    Claim 1; SEQ ID 2300; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC02302 standard; cDNA; 441
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggtgggcacctcggcgggggtggtcc
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441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag; secreted protein; cDNA isolation; phromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122487
102 A; 130 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.5%;
                                                                                                                                                                                                                                                                                                                                                                 Duclert
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 122
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87
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RESULT 1
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                                                                                                                                                                                                                                                    vulnerary; nootropic; anti-HIV; neuroprotective; antibacterial; ds;
cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic
                                                                                                                                                                                                                                                                       Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic; Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
                                                                                                                                                                                                                                                                                                            Mouse RetL5
                                                                                                                                                                                                                                                                                                                                                                           AAF57269 standard; DNA; 15914 BP
                                                                                                                                                                                                                                                                                                                                                        AAF57269
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                                                                                                                                                                                                                                                                                                                                                                                                                                   158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGGNCAGNAGNAANGGANTTGGNCCCAACCCCNTTGGTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcgaagtggcgcggctgttggccagcagtgatccactggcccagatcgcagaggacaagc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGNCCTGGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTC
                                                                                                                                                                                                                                                                                                           genomic
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                          DNA sequence
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Mus sp WO200116169-A2

08-MAR-2001

01-SEP-2000; 2000WO-US24111

01-SEP-1999; 99US-0152024

(BIOJ ) BIOGEN

Worley

2001-235091/24

Novel Ret ligand polypeptide useful for suppressing growth of a tumor cell that expresses Ret and for modulating Ret signal transduction involving a cell expressing Ret polypeptide or Ret ligand polypeptide

Claim 1; 76pp; English

The invention relates to mouse and human Ret ligand 5 (RetL5) polypeptides. The RetL5 polypeptides can be expressed by standard recombinant methodology. The RetL5 when bound to Ret, acts as a dimerization or autophosphorylation activator. The polypeptides and their antibodies are useful for stimulating growth of or limiting damage to, Ret expressing tissue in a subject, for suppressing growth of a tumour cell that expresses Ret, for modulating Ret signal transduction involving a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion proteins containing RetL5 and antibodies are useful for stimulating renal tissue growth and/or survival, supporting renal function and minimizing damage to renal tissue after various insults, particularly for treating acute renal fallure, acute nephritis, chronic renal fallure, nephrotic syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic injury and trauma. The compounds are also useful for treating conditions are also useful for treating conditions and account of the compounds are also useful for treating conditions and compounds are also useful for treating conditions are also useful for treating conditions are also useful for treating conditions are a tissue caused by neoplastic impingement, trauma or cerebrovascular events such as hemorrhage or emboli, and neural disorders such as mental retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral motor neuron disease, demyelinating disease, bacterial diseases, viral diseases, and prion diseases including Creutzfeldt-Jakob disease. The compounds are also useful for treating disorders due to damage to neural such as neural degeneration where neural growth and regeneration are desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as present sequence genomic DNA sequence 01

infection

transgenic plants

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          DNA-B. It encodes a protein (see AAW34336) having a DNA binding site specific to the DNA-A common region, a DNA nicking activity, and an NTP binding activity. The invention involves production of transgenic plants containing DNA comprising AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with
                                                                                     This genomic DNA sequence includes the open reading frame of the wild-type ACl gene of tomato mottle virus (TOMOV), a geminivirus that has a bipartite genome. The ACl gene must be expressed for
                                                                            that has a bipartite genome. The AC1 gene must be exefficient replication of the two genomic components,
                                                                                                                                                    Example 3.3;
                                                                                                                                                                               golden mosaic
                                                                                                                                                                                        Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
                                                                                                                                                                                                                                               P-PSDB; AAW34332
                                                                                                                                                                                                                                                                                          Ahlquist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geminivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomato mottle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT93294;
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                                                                                                                                                                                                                                                                                                                     (SEMI-) SEMINIS VEGETABLE SEEDS INC (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                               16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAGNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTCTGTCTGTACAAGGTGCTACTAAGTTTGTTTTTATTATTTGACTGTTTTGGTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACAGGGTTTCCTCTGTGGGCCCTAGCTATCCTGGAACTCAATCTGTAGACCAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mottle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                         PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s; ToMoV; AC1 geplant; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                    Page 57-58; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                               geminivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus isolate Florida
                                                                                                                                                                                                                                                                                          Hanson
                                                                                                                                                                                                                                                                                                                                                                                         97WO-US06300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC1
                                                                                                                                                                                                                                                                                          SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    open
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                                                                                                                                                                                                                                                                                          Luu HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reading
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transdominant mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                          Maxwell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; cyclic; circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
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                                                                                                                                                                                                                                                                                          Stout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                               DNA-A and
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Best Local
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         This DNA sequence comprises a mutated ACl gene of tomato mottle virus (TOMOV). It carries an inserted 4-base Sau3A site that shifts the ACl gene translation reading frame resulting in the expression of a truncated ACl protein (see AAM3437). The ACl gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants
                                                                                                                                                             Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
                                                                                                                                                                                                                                                                                       (SEMI-)
                                                                                                                                                                                                                                                                                                                                                           15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geminivirus; ToMoV-Acidlm23; AC1 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are resistant to viral infection. The AC1/C1 genes are especially from ToMoV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAM33282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking domain and/or the NTP-binding domain.
 genome. The in
containing DNA
                                                                                                                        Claim 11; Page 72-73;
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P-PSDB; AAW34327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomato mottle virus isolate Florida
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                                                                                                                                                  golden mosaic geminivirus
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nvention involves production of transgenic plants comprising geminivirus ACl or Cl wild-type or mutant
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Pred. No. 3.9;
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virus (ToMov). It encodes an Acl protein (see AAW34324) that carri mutations in its NTP-binding domains. The Acl gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A-and DNA-B, of the bipartite ToMov genome.
                                                                                                                          Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
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                                                This DNA sequence comprises a transdominant lethal mutant, designated ToMoV-AC1dlm, of the AC1 gene of tomato mottle virus
                                                                                        Claim 11;
                                                                                                              golden mosaic geminivirus
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The invention involves production of transgenic plants containing DNA comprising geminivirus ACl or Cl wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The ACl/Cl genes are especially from ToMOV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93288-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding
                                               domains.
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Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 other;

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US-08-943-768-1
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US-08-913-309A-5
US-08-314-309A-3
US-08-314-309A-3
US-08-313-594-1
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Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 49, Appl	Sequence 218, App	Sequence 51, Appl	Sequence 28, Appl	Sequence 28, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 48, Appl	Sequence 21, Appl	Sequence 8, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 16, Appl

ALIGNMENTS

## RESULT 1 PCT-US95-11684-1/c Sequence 1, Application PC/TUS9511684 GENERAL INFORMATION: EILING DATE: 14-SEP-1995 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION UNMBER: US 08/308 FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION: NAME: LOGAN, APPILC. REGISTRATION NUMBER: 33,950 REFERENCE/DOCKET NUMBER: BECO COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/11684 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937 TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 1: APPLICANT: THE SCRIPPS RESEARCH INSTITUTE TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND TITLE OF INVENTION: AND USING SAME NUMBER OF SEQUENCES: 28 SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS FEATURE: MOLECULE TYPE: STREET: 10666 CITY: La Jolle STATE: CA COUNTRY: USA ZIP: 92037 NAME/KEY: CDS LOCATION: 55..665 OTHER INFORMATION: LENGTH: 7286 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ADDRESSEE: The Scripps Research Institute, Office ADDRESSEE: Patent Counsel STREET: 10666 North Torrey Pines Road, TPC 8 Jolla DNA (genomic) /product= "cytotactin" PCT/US95/11684 08/308,359 BEC0019P Version #1.25 of. METHODS OF MAKING

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Best Local Similarity
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ENERAL INFORMATION:
    1152
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                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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APPLICANT: Sima Lev

APPLICANT: Joseph Schlessinger

APPLICANT: PYK2 RELATED PRODUCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                             114 CTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGT 173
                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
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                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                        STRANDEDNESS: single
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ZIP: 90071-2066
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STREET: Suite 4700
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CTATGAGGTCAGCCATGTTCTCAGCCTCTGCTAGGGATGAGGTTTTGATGGACAAGGCCT 1093
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                                                                 54;
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                                                                                                                                                                                                         nucleic acid
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48.6%;
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52.9%;
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                                                                               Score 28.2; D
Pred. No. 2.4;
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Pred. No. 3.
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                                                                Mismatches
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                                                                                             DB 2;
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                                                                                            Length 3416;
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                                                                                                                                  Matches
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Best Local
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1092 GGGGGGCACCTTCAATGCCCAGCTGAAGTACTGCCTGGCCCT 1051
                                                                  1152 CTATGAGGTCAGCCATGTTCTCAGCCTCTGCTAGGGATGAGGTTTTGATGGACAAGGCCT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: IBM
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/357,642
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TITLE OF INVENTION: PYK-2 RELATED PRODUCTS
TITLE OF INVENTION: METHODS
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APPLICANT: JOSEPH SO
                   174 GGGÀGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCT 215
                                                                                               114 CTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGT 173
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                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
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STREET: Suite 4700
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67-3510
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                                                                                                                               Score 28.2; DE Pred. No. 2.4; 0; Mismatches
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                                                                                                                                                                  Length 3416;
                                                                                                                                Indels
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US-09-422-869-1 ; Sequence 1, Application US/09422869 ; Patent No. 6235481

GENERAL INFORMATION:

APPLICANT: POLONSKY, KENNETH S.

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Best Local Similarity 53.8%;
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SEQ ID NO 1
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CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
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APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                       REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 940 base pairs
                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Grierson, Alastair
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ZIP: 98121
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                         206-269-0563
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Pred. No. 1
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                                                                                                                   US-08-975-316-3
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                                          Matches
                                                         Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: BLOKSBERG, Leg
APPLICANT: and GRIERSON,
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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232 CTGGTCGTCCCATCGCCTAGCAGGGGTTCAAGNAAAGGGGGCCCGCNCATGGCAGTCCTTGG 291
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                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                  TOPOLOGY:
                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                          Conservative
                                                                                                                                   linear
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Pred. No. 2.7;
                                                         Score 27.2;
Pred. No. 2.
                                          Mismatches
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                                                                       DB 2;
                                          52; Indels
                                                                       Length 940;
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                                                                ZIP: y430*****
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F4855EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
***TOATION NUMBER: US/08/911,853
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Best Local Similarity
       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/699
APPLICATION TO NUMBER: 16-AUG-1996
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LOCATION: (463)...(463)
-09-211-710-3
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APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000,1003C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/211,710A CURRENT FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, Leonard N
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pinus radiata
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                     CITY: Palo Alto
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925 Page Mill Road
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                                   08/699,092
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US-09-479-409-6
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Best Local (
                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Gerrit
APPLICANT: Quax, 1
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                                                                                                                   REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 33,888
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                         STRANDEDNESS:
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                                                                                                      TELEPHONE:
                                                                                                                                               NAME: Glaister, Debra REGISTRATION NUMBER:
                                                    LENGTH:
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                               FILING DATE
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                                    nucleic acid
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EDNESS: single
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Quax, Wilhelmus J.
Quax, EXPRESSION S
                                                 1512 base pairs
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925 Page Mill Road
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Pred: No. 3
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Query Match

Best Local Similarity

8.1%; 60.3%;

Score 27.2; D Pred. No. 3.5;

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...RESULT 11
US-08-911-853-29
· Sequence 29, Application US/08911853
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Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BLOKSBERG, LEGISLATINE.
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
                                                                                                                                                                   1041 CTGGTTCCGTTATCTGCACGCCTGGTCCAAGAACAGCGTCCAGCCTCTGCGCGCACCTTGC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                         186
                                                                                                                                                                                                    232
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                                                                                                                                      292 NCAGNAGNAANGGANTTGGNCCCAACCCCNTTGGTTCCCAACCCA 336
                                                                                                                                                                                                                                    Local Similarity
les 53; Conserv
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/975,316 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                        TCTGAATGTCCTGGTGGTTCACCAGCTCCGCTATTCCCCATTCCA 937
                                                                                                                                                                                                   CTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCCGCNCATGGCAGTCCTTGG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGCGCC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAAGGCATCGGCCAGACCCAGGTCAACCCCGCGGGTGGACATGACCTTCGCCCGCGGCC 955
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                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            1785 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                              206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                              8.1%;
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Pred. No. 3.9;
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                                                                                                                                                                                                                                                                DB 2;
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RESULT 12
US-09-479-409-29
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                                                                                                                                                                                                                                             Sequence 29, Appli
Patent No. 6225106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699
APPLICATION 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             11077
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: APPLICANT ON: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM
                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                           APPLICANT: Gerritse, Gijsbert APPLICANT: Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                            233 TGGTCGTC 240
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OPERATING SYSTEM:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 33
                                                                   STATE:
                                                                                STREET: 925 Page
CITY: Palo Alto
                                                                                                ADDRESSEE: Genencor International STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/911,853
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94304-1013
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nucleic acid
                                                           CA
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                                                                                                                                                                                                                                                             Application US/09479409
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Diskette
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                                                                                                                                                 EXPRESSION 37
                                                                                                                                                                             EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/699,092
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Pred. No. 14;
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                                                                                                                                                              SYSTEM FOR ALTERED LEVELS
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Gaps

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SUFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:

2.0

OPERATING SYSTEM:

IBM Compatible

APPLICATION NUMBER: US/09/479,409

FILING DATE:

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         В
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                                                                                                                             Matches
                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 17949
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09087465A Patent No. 6160092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/087,465A CURRENT FILING DATE: 1998-05-29
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Darnell Jr., James E
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: USE
                                                          12998 aaaaaaaaaaagtgctgttcatctgtgtgatctcactgaatcttcgtacttcaaaccct 13057
SOFTWARE:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 600-1-229
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Xiaomin
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11017 TGGAAGGCATCGGCCAGACCCAGGTCAACCCGCGGGTGGACATGACCTTCGCCCGCGGCC 11076
                              220 TTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCAT 279
                                                                            160 AAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGUNTGGCCCTGAGN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
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REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGCGCC 11084
                                                                                                                              66;
                                                                                                                                                                                                                                                                             PatentIn Ver. 2.0
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                                                                                                                             Conservative
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                                                                                                                                         8.0%;
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                                                                                                                                        Score 27;
Pred. No.
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Pred. No. 1
                                                                                                                           Mismatches
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                                                                                                                                        DB 4; Length 17949; 17;
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                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17612;
                                                                                                                         Indels .
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                                                                                                                      Gaps
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                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1329 bases
                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Dell 486/50
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Squinto, Stephen P.
TITLE OF INVENTION: Retroviral
TITLE OF INVENTION: Expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                          VOLUME: 64
TAGES: 5491-5499
                                                                                                                                                                                                                    TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kiee, Maurice M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: July 2
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 GGCAGTCCTTGGNCAGNAG 298
                                                                                                                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleic acid
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: Coppola, M. A.
: Thomas, C. Y.
Origin of pathogenic
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Xenotropic gp70
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Score 26.4; DI
Pred. No. 6.5;
0; Mismatches
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Matches

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; TOPOLOGY: 11r; MOLECULE TYPE: ; HYPOTHETICAL: NO ; ANTI-SENSE: NO US-08-848-810-1
Search completed: August 24, 2001, 03:51:27 Job time: 2333 sec
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Best Local Similarity 48.6
Matches 54; Conservative
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Patent No. 6074851
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Yem, A. V
APPLICANT: Wilson, of
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WOOLTON, Thomas A.
REGISTRATION UNBER: 35,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,810
FILING DATE:
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MEDIUM TYPE: Floppy disk
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Post-processing: Minimum Match 0%
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                          Bovidae; Bovinae; Bos.
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Sugimoto,Y., Hirotsune,S.,
                                                                                                               COW.
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
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                                                                                               Bos taurus
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 cDNA sequencing
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Bos taurus kidney fetus
sequence.
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                           Takasuga, A.,
                                                                                                                                                                                   Bos taurus
                             Itoh, R.,
                                                                                                                                                                               30-AUG-2000
CDNA clone E1KI043F08
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BF138468 601782924
BB040208 BB040208
BE304035 601084682
BF159013 601766324
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BF300893 602028894
AA998476 UI-R-CO-i
AA997859 UI-R-CO-h
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AL26069 Tetraodon
AA234493 zr74h07.r
BF076427 225993 MA
BF47871 602023024
BG472715 60254536
BE37875 601237207
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BF325039 Su1Bg10.y
BF077799 227942 MA
BF077938 229798 MA
AW405671 UI-HF-BK0
A1856977 MBNAAd-05
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AW596813 sj83a05.y
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AV663492 AV663492
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BE121364 UI-R-CA0-
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BF394149 UI-R-CA0-
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                                                                      Bovoidea;
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                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                           AUTHORS
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AV663493.1
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AV663493
5', mRNA
                                                       Single pass sequencing. This clone was obtained from
                                                                                                                                                                   Unpublished (2000)
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos. 1 (bases 1 to 539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing.
This clone was obtained from
Location/Qualifiers
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                                                                                                                                                                                                                        Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kazusugi@cocoa.ocn.ne.jp
                                                                                Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                       Location/Qualifiers
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/db_xref="taxon:9913"
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-Shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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116 c 157 g 110 t 1 others
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polyA-deleted cDNA library.
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JOURNAL
      Matches
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Unpublished (2000)
Contact: Yoshkazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA
AV663814
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AV663814
5', mRNA
                                                                                                                                                                                                                                      Single pass sequencing. This clone was obtained from a polyA-deleted cDNA library.
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    Conservative
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/db_xref="taxon:9913"
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/lab_host="DH10B"
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a 144 c 129 g 128 t
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/dev_stage="fetus"
/lab_host="T0H10B"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
133 c 123 g 126 t
                                                                                                                                                                                                                                                                                                                                                                                                                       1 to 539)
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               24.48;
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89.4%;
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    0;
             Score 82; DB 32;
Pred. No. 4.3e-15;
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Pred. No. 4.3e-15;
0; Mismatches 11
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                           Length 539;
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  Indels
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 ATT
                                                                                                               108;
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                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                             Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
AU135898
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AU135898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 796)
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HRI human cDNA project
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/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME185FL3"
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/db_xref="taxon:9606"
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Mammalia; Eutheria; P
1 (bases 1 to 900)
Li,W.B., Gruber,C., J
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AL541183 LTI_FL002_PL1 Homo
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Unpublished (2001)
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EST.
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AL537924 LTI_FL013_FBrn1
prime, mRNA sequence.
AL537924
                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Tife.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_llb="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from
week, 24 week and 26 week)
/lab_host="DH10B"
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il c 224 g 245 t
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Pred. No. 6.8e-14;
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 and Polayes, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 106;
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Genoscope - Centre National de S
BP 191 91006 EVRY cedex - France
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                                                                                                             Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                            USDA, ARS, US Meat Animal
PO Box 166, Clay Center, I
Tel: 402 762 4366
Fax: 402 762 4390
                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 2:
                                                                                                                                                                                                                                                EST discovery in swine Unpublished (2000)
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                                                                FORWARD: AGGAAACAGCTATGACCAT
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                                                                                            and -minmatch 12 options.
                                                                                                                                                                                                                                Contact: Smith TPL
                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                                                     and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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238 c 213 g 222 t
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/db_xref="taxon:9606"
/clone="CSODE005YD14"
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/lab_host="DH10B"
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             row: K column: 23
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8.9e-14;
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                                                                                                                                                                                                                                                                                                                               Email: msoareseblue weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message.cDNA Library Preparation: M.E
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                           Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                            Research Genetics (www.resgen.com)
Seq primer: M13 Forward
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Rattus norvegicus
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           /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library
                                                                                                                                             /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA0-bax-a-08-0-UI"
/clone_lib="UI-R-CA0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2:
Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
                                                                                                                                                                                                                     organism="Rattus norvegicus"
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/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
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/lab_host="DH10B"
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which this clone was
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88.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
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Tel: 319 335 8250
Fax: 319 335 9565
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
/Clone_"U.T. CAO."
/clone_Tib="UITA-CAO."
/clone_Tib="UITA-CAO."
/lab_host="DHIOB (Life Technologies)"
/lab_
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TAG_SEG-None found*
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80.5%;
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Pred. No. 5.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 Eckstein Medical Research
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery
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Rattus norvegicus
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                /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
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previously described in (Bonaldo,
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                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                               /clone_lib-"UI-R-CAO"
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80.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: nouse.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602390647F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502603 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG293757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAM10371 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nmalia; Eutheria; (bases 1 to 711)
                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
Location/Qualifiers
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                                                                                                                             /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4502603"
/clone=lib="NH_MGC_94"
/tissue_type="retina"
/tissue_type="retina"
/lab_host="PH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pcMV-SPORT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D
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TAG_SEQ=None found"
106 c 117 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
   16.7%;
84.9%;
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lence stop: 708.
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Rodentia;
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Pred. No. 5.2e-09;
Score 56; DB 175;
Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian Gene Collection (MGC)
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                            DB 175;
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                         Length 711;
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AV663813/c
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JOURNAL
                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                  414 ACAGCAAAACAGAGAGCTCAT-TCATGATGGACTCGGATCCTCAACG-CTGCATGAGGCA 357
                                                                                                                                                                           356
                                                                                                                                                                                                 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                        CCACTATGTTGATT
                                                                                                                                                                                        CCACTATGTTGNAT 124
                                                                                                                                                                                                                               ACAGCAAAACGGACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCA 110
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                                                                                          BF300893 938 bp m
602028894F1 NCI_CGAP_SG2
                                                                                                                                                                                                                                                                         63;
                       Mus musculus
                                                   EST
                                                           BF300893.1
                                                                         BF300893
           Eukaryota;
                                     ouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
1 (bases 1 to 414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV663813 414 bp mRNA
AV663813 Bos taurus brain fetus
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV663813
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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                                                                                    sequence
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone was obtained from a polyA-deleted cDNA library
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                                                                                                                                                                                                                                                                                                                                          /note="Vector: pZL1; Site_1:
was deleted from a Not1 site"
    112 c    133 g    82 t
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9913"
/clone="E1BR038G07"
/clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
         Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                              'dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Bos taurus"
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                                                                                               musculus
         Craniata;
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                                                                                                                                                                                                                                                                                            DB
                                                                                              CDNA
                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                  Sall; Site_2: Not1; Poly A
                                                                                                                                                                                                                                                                   9;
       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh, R.,
                                                                                             clone
                                                                                                                                                                                                                                                                                           Length 414;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961-8061,
                                                                                          IMAGE:4164238 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jitohzono, A.
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                                                                                                        21-NOV-2000
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AUTHORS
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SOURCE
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VERSION
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TITLE
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Best Local :
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                                                                                                                                                                                                                                                                                                                          TAAGTCCCGAGCCCA
                                                                                    1 (bases 1 to 330)
1 (bases 1 to 330)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                       Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                   97044477
On Jun 5, 1998 this
                                                                       Genome_Res. 6 (9), 791-806 (1996)
                University of
                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 68; Conser
                                                                                                                                                                Eukaryota;
                                                                                                                                                                                      Norway rat.
                                                                                                                                                                                                                AA998476.1
                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999
Eckstein Medical Research Building Iowa City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases
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                                                                                                                                                   Eutheria;
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                                                                                                                                                                                                                GI:4290126
                Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%;
                                                                                                                                                  Chordata;
Rodentia;
                                                 sequence version replaced
                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
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approaches

ç

facilitate

gi:3189127

IA 52242, USA

Muridae;

Euteleostomi; Murinae;

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806 GAAAGAAGTCCGCCCCTGGGAAACCATTGGAATGAGATAAGCAGTTGCCCAGAAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 GNAAAGGGGCCCGCNCATGGCAGTCCTTGGNCAGNAGNAANGGANTTGGNCCCAACCCCN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 CCCCGNNTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAA 261
AA998476 330 bp mRNA EST UI-R-CO-ie-a-08-0-UI.S1 UI-R-CO Rattus norvegicus UI-R-CO-ie-a-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: LLAM9449 row: k column: High quality sequence stop: 686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9449 row: k column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4164238"
/clone_lib="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: Size align: pCMV-SPORT6; Site_1:
/note="Organ: Size align: pCMV-SPORT6; Site_1:
/note="Organ: pCMV-SPORT6
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/strain="FVB/N"
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1 to 938)
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Pred. No. 1.3;
0; Mismatches
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cDNA clone
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Locus
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 TGCTCCTGCTGCTGCTGCTTCAGGGGGGACTCAACACTGGCAAGCCATCTTCTG 200
                                                                                                                                                                                                                                                                                               138 CCGTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                              78 ATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCAC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 TGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTCGTNTCATG 77
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AA997859 519 bp mRNA EST UI-R-CO-hu-c-11-0-UI.s1 UI-R-CO Rattus norvegicus UI-R-CO-hu-c-11-0-UI 3', mRNA sequence.
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/note="Vector: pf773D-Pac (Pharmacia) with a modified
/note="Vector: pf773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Bco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-Al
and UI-R-EI libraries. The UI-R-AI library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placentd, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-A1 and UI-R-EI clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-A1 and UI-R-EI library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
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/clone_lib="UI-R-CO"
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Pred. No. 1.6;
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Query Match 10.6 Best Local Similarity 54.4 Matches 68; Conservative

10.6%;

Score 35.6; DI Pred. No. 1.8; 0; Mismatches

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14; 57;

Length 519; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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Program for Rat Gene Discovery and Mapping
University of Iowa
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence tag present
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                                                                                                                                                                                                                                                                                                              embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of the pooled UI-R-A1 and UI-R-E1 library in the form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; The UI-R-CO library is a subtracted library derived from the UI-R-Al and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day normalized libraries constructed from 8, 12 and 18-day
                                                                                            bacteria (Life Technologies) to generate the UI-R-CO Library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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                                                                 1996)"
                                                                                                                                                                                             hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B
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/db_xref="taxon:10116"
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Title:
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

C 321	Result
2222223	Score
55555555555555555555555555555555555555	% Query Match
1769 1774 1846 1872 119945 162409 1493 1792	% Query Match Length DB
94 93 93 91 91	Dв
MMNDP MMNORRIE HSNDPG HSCHRX HSCA218J18 AC022184 BC006263 AF236018	ID
X83794 M.musculus X92397 M.musculus X92397 M.musculus X65882 H.sapiens m X65724 H.sapiens D ALO34370 Human DNA ACO22184 Homo sapi BC006263 Homo sapi AF236018 Cercopith	Description

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                                       Submitted (05-JAN-1995) z. Chen, Molecular Neurogenetics Lab, Massachusetts General Hospital-East, Building 149, 13th Stree Charlestown, MA 02129, USA Location/Qualifiers
                                                                                                               Characterization and mapping of
                                                                                                                                                                                        MMNDP 1769 bp
M.musculus NDP gene.
X83794
                                                                        Direct Submission
                                                                               Chen, Z
                                                                                             96432457
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Battinelli,E.M., Boyd,Y., Craig,I.W., Breakefield,X.O. and
                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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NDP gene; Norrie disease locus.
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                                                                                                   Genome 7
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Direct Submission
Direct Submission
Submitted (17-OCT-1995) W. Berger, MPI fuer Molekulare Genetik,
Ihnestrasse 73, D-14195 Berlin, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; N (bases 1 to 1774)

Berger, W., van de Pol, D., Bachner, D., Oerlemans, F., Winkens, H., Hameister, H., Wieringa, B., Hendriks, W. and Ropers, H.H. An animal model for Norrie disease (ND): gene targeting of the
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X92397
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/chromosome="X"
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ALRLRCSGGMRLJTATYRYILSCHCEECSS"
1744. 1749
                                                                                   join(432. .599,600. .827)
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                                                                                                                                                                                                                         tissue_type="brain"
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/clone_lib="FIXII phao
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/note="Norrie disease
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X65882 S61557
X65882.1 GI:35016
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                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 1 (3), 204-208 (1992)
93265104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1872)
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/db_xref="GI:1335017"
/translation="RHGGCDAGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
/translation="RHGGCDAGACDSLPSTGTSSPVTARNAIPEARCCVWLLDGTTV
EAVRPARERLAKKELROKKMOOFSRDSAYSSNKDSTCLLTEROTLGTSLOFFSPFSGT
ISFGSFSDSGIFPLGSOCCLGFOQFSISGKKWALIHKRVRLSVFGARWGRIYFGK"
1 425 c 409 g 517 t
                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA46639.1"
/protein_id="CAA46639.1"
/db_xref="GI:29947"
/db_xref="SWISS-PROT:000604"
/db_xref="SWISS-PROT:000604"
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/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDSISHPLYKCSSKMYLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
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conceptual translation"
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/db_xref="taxon:9606"
/chromosome="X"
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/map="pll.4"
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P.O.Box 9101, 6500 HB
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twiere's differences are found these are annotated as variation together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  HMCORTANT: This sequence is not the entire insert of clone 218118. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between the true right end of clone 27K14 (299125) is at 100 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome X. Gonstructed by the Sanger Contre through the library RPCI6 constructed at the Roswell Park Generi Institute by the group of Pleter de Jong. For further Generian Stitute by the group of Pleter de Jong. For further Contre Note: "MEDIB repeat: matches 1394 of consensus" region 1840. 1895  111994  / Clone_lib="RPCI-6"  / Chromosome="X"  / Conce:"REF-218118  / Colone_lib="RPCI-6"  / Chromosome="X"  / Conce:"REF-218118  / Colone_lib="RPCI-6"  / Chromosome="X"  / Chromosome="X"  / Choice:"REF-218118  / Colone_lib="RPCI-6"  / Chromosome="X"  / Choice:"REF-218118  / Colone_lib="Ref-218118  / Colone_lib="Ref-218118  / Colone_lib="Ref-21818  / Colone_lib="Ref-2181	Submitted (26-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clonests: clonerequest@sanger.ac.uk	Metazoa; Chordata; Craniata; Vertebr Eutheria; Primates; Catarrhini; Homin I to 119945)	sequence. Sequence. Sequence. Sequence. Sequence. Sequence. Sequence. AL034370 AL034370.1 GI:3947696 HTG; CC1.3 Splicing Factor; NDP; Norrie Disease; Pseudoglioma. human. Homo sapiens	HSA218J18 119945 bp DNA PRI 23-NOV-1999 Human DNA sequence from clone 218J18 on chromosome Xpl1.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains FSTs. STSS and GSGs complete
repeat_region	repeat_region	repeat_region repeat_region repeat_region	repeat_region repeat_region repeat_region	repeat_region repeat_region
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"match: proteins 000604 P48744"
                                                                                                                                   ement(29013. .29019)
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uct="NDP (Norrie Disease (Pseudoglioma))"
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724 AA670439 W61129 N59262 AA045724 AI129296 W61167
L R84741 H85821"
                                                                                                                                                                                                                                              ment(28998.
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ment(join(28998. .30248,38694. .39074,53526. .53726))
"NDP"
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.14986
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.14210
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"MIR repeat: matches 20.
.13006
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                                                                                                                                                                   AC022184 162409 bp DNA
Homo sapiens chromosome 4 clor
SEQUENCE, 12 unordered pieces
                                                AC022184.3 GI:10047716
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/note="MIR_repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LlP4 repeat: matches 5408.
42540. .43017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="31 copies 2 mer ag 90% conserved" 56812. .57069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2589. .2709 of
53680. .53741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 56. .142 of consensus"
45355. .45652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 20.
41308. .41535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40405.
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/note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="16 copies 2 mer ac 100% complement(33360. .33924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="26 copies 2 mer aa 73% conserved" 31354. .31662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER5B repeat: matches 58. .178 of consensus"
30652. .30703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA22268.1"
/db_xref="GI:3947697"
/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDS1SHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1M4b repeat: matches 154. .237 of consensus"
44932. .45016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 2579. .2698 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS AQ042323"
33571. .33727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: STS AF020217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="15 copies 2 mer aa 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2646. .2741 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="FAM repeat: matches l. .173 of consensus"
33007. .33238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluJo repeat: matches 1. .308 of consensus"
32205. .32377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluJb repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="match: EST AA779268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MER5A repeat: matches 9. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L2 repeat: matches 2177. .2417 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .35714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .43506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .48194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 92;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                       clone RP11-52G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .213 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .262 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .248 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .244 of consensus"
                                                                                                                                                                                                                       map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5640 of consensus
                                                                                                                                                                                                                            WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Colaryki, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Feizhugh, W., Forrest, C., Gage, D., Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., Machaers, T., Lehoczky, J., Mervine, R., Lieu, C., Liu, G., Locke, K., Macdonaid, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., Machaers, R., Meddrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Petterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dispar, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced g1:7107809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 162409)
Birren, B., Linton, L.,
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150598 bases at least Q40
Consensus quality: 156229 bases at least Q30
Consensus quality: 158583 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 161309; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                      6777: contig of 6777 bp in length 6878 6877: gap of 100 bp 68136: contig of 1250 
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Center clone name: 52_G_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center Center code: WIBR
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                                                                                                                                                                                                                       12553 12652:
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                                                                                                                                                                                978 8136: contig of 1259 bp in length 137 8236: gap of 100 bp in length 97 10036: gap of 1760 bp in length 97 10036: gap of 100 bp 17552: contig of 2456 bp in length 13 12652: gap of 100 bp 13 2652: gap of 100 bp 20126: gap of 100 bp
27970: contig of 7844 bp
28070: gap of 100 bp
36727: contig of 8657 bp
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KEYWORDS
SOURCE
ORGANISM
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BC006263
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ORIGIN
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                                                                                                                                                                                                                                                                                     Local Similarity
nes 22; Conserv
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       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1493)
                                                                                              Homo sapiens, Similar to diacylglycerol homolog, clone IMAGE:3949350, mRNA, part BC006263
BC006263.1 GI:13623318
                                                    Homo sapiens
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51073 68989: contig of 17917 bp in length
68990 68989: gap of 100 bp
69090 91875: contig of 22786 bp in length
91876 91975: gap of 100 bp
91976 129030: contig of 37055 bp in length
129031 129130: gap of 100 bp
129131 162409: contig of 33279 bp in length
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91976. .129030
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8237. .9996
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/db_xref="taxon:9606"
/chromosome="4"
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                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Cercopithecus
African green monkey.
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon;C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, L.-H. and Green, E.D.
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaithersburg, Maryland;
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Tissue Procurement: DCTD/DTP
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(mouse) homolog"
/protein_id="AAH06263.1"
/db_xref="gci:18623319"
/translation="GTRLNWCVVMLILSNARLFLENLIKYGILVDPIQVVSLFLKDPY
/translation="GTRLNWCVVMLITTH"
/translation="GTRLNWCVMLITTH"
/transla
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/clone_lib="NIH_MGC_9"
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/db_xref="taxon:9606"
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Pred. No. 1.7;
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                                                                                                                                                                                 mRNA PRI 12-AU diacyl-glycerol acyltransferase
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Sequence 32
AX090339
AX090339.1
                                                                                                                                                                                                                       synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1895)
Lassner, M. and van Eenennaam, A.
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Submitted (17-FEB-2000) Pathology,
University School of Medicine, Medi
NC 27106, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                Plant sterol acyltransferases Patent: WO 0116308-A 32 08-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1792)
Joyce, C.W., Davis, M.A., Anderson, R.A. and Rudel, L.L.
                                                                                                                                                                                       MONSANTO COMPANY (US)
                         Similarity
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LIMLIFEYWLEHSCLNAVAELMOFGDREEYRDMWLSESVTYEMQNWNIPVHKWCIRHE
YKPMLRRGSSRWMARIGVFLASAFFHEYLVSVPLRWFRLWAFTGMMAQIPLAWFVGRF
EQGNYGNAAVWLTLIIGGPIAVLMYVHDYYVLNYEAPVAGA"

572 c 534 g 389 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Inferred cDNA
                                                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
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/db_xref="taxon:9534"
/tlssue_type="liver"
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                                                                                                  /note="n=unknown"
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Direct Submission
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AF059202
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                        Homo sapiens
                                                            X97675.1 GI:1834512
                                                                         H.sapiens mRNA for plakophilin x97675
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Location/Qualifiers
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/note="ARGP1"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1976)

Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.L. Characterization of two human genes encoding acyl coenzyme A:cholesterol acyltransferase-related enzymes

J. Biol. Chem. 273 (41), 26765-26771 (1998)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYGNAAVWLSLIIGQPIAVLMYVHDYYVLNYEAPAAEA"
1712. .1976
a 639 c 616 g 398 t
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/product="AcA" related gene product 1"
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LFLENLIKYGGILVDPJOVYSLFLKDPHSWPACPLVIAANVFAVAAFOVEKRLAVGALT
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RRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYTLFAPTLCYELMFPSRIRKR
RRARKAASAGKKASSAAAPHTVSYPDNLTYRDLYYTLFAPTLCYELMFFRSRIRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLLRRILEMLFFTQLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIW
LIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKP
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Plakophilins 2a and 2b: constitutive proteins of dual location
the karyoplasm and the desmosomal plaque
J. Cell Biol. 135 (4), 1009-1025 (1996)
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Location/Qualifiers
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Revised by [3]
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Submitted (29-APR-1996) C. Mertens, German Cancer Research Center,
Cellbiology, Im Neuenheimer Feld 280, Heidelberg, 69120, FRG
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Conservative
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QLRGIIKLLQLLKVQNEDVQRAVCGALRNLVEEDNDNKLEVAELIGVPRLLQVKQTR
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KYSQNIYIQNRNIQTDNNKSIGCFGSRSRKVKEQYQDVPMPEEKSNPKGVEWLWHSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHNLSYQLEAELPEKYSQNIYIQNRNIQTDNNKSIGCFGSRSRKVKEQYQDVPMPEEK
SNPKGVEWLWHSIVIRMYLSLIAKSVRNYTQEASLGALQNLTAGSGPMPTSVAQTVVQ
KESGLQHTRKMLHVGDPSVKKTAISLLRNLSRNLSLQNETAKETLPDLVSIIPDTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTHSDYQYSQRSQAGHTLHHQESRRAALLVPPRYARSEIVGVSRAGTTSRQRHFDTYH
RQYQHGSVSDTVFDSIPANPALLTYPRPGTSRSMGNLLEKENYLTAGLTVGQVRPLVP
LQPVTQNRASRSSWHQSSFHSTRTLREAGPSVAVDSSGRRAHLTVGQAAAGGSGNLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="maapgapaeygyirtvlgQQilgQldSSSlalpSEAKLKLAGSS
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PVPKTYDMLKAGTTATYEGRWGRGTAQYSSQKSVEERSLRHPLRRLEISPDSSPERAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVPKTYDMLKAGTTATYEGRWGRGTAQYSSQKSVEERSLRHPLRRLEISPDSSPERAH
YTHSDYQYSQRSQAGHTLHHQESRRAALLVPPRYARSEIVGVSRAGTTSRQRHFDTYH
RQYQHGSVSDTVFDSIPANPALLTYPRPGTSRSMGNLLEKENYLTAGLTVGQVRPLVP
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DIFYNVTGCLRNMSSAGADGRKAMRRCDGLIDSLVHYVRGTIADYQPDDKATENCVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERSTFTDSQLGNADMEMTLERAVSMLEADHMPPSRISAAATFIQHECFQKSEARKRVN
QLRGILKLLQLLKVQNEDVQRAVCGALRNLVFEDNDNKLEVAELNGVPRLLQVLKQTR
                                                                                                                                                                        YKKAQFKKTDFVNSRTAKAYHSLKD"
1005 c 976 g 1022 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="plakophilin 2b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDLLIETTASACYTLNNIIQNSYQNARDLLNTGGIQKIMAISAGDAYASNKASKAASV
LLYSLWAHTELHHAYKKAQFKKTDFVNSRTAKAYHSLKD"
                                                                                                                                                                                                                           GDPSVKKTAISLLRNLSRNLSLQNEIAKETLPDLVSIIPDTVPSTDLLIETTASACYT
LNNIIQNSYQNARDLLNTGGIQKIMAISAGDAYASNKASKAASVLLYSLWAHTELHHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {f GRGGQTVKSLRIQEQVQQTLARKGRSSVGNGNLHRTSSVPEYVYNLHLVENDFVGGRS}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQPVTQNRASRSSWHQSSFHSTRTLREAGPSVAVDSSGRRAHLTVGQAAAGGSGNLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:Q99959"
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                        Score 20;
Pred. No.
   Mismatches
                           DB 93;
1.7;
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Jun 1, 2000 this sequence version replaced gi:6531668.

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arrively. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wen,G., Siebert,R., Schilhabel,M.B., Chromosome 8 genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF205589 133075 bp DNA HTG 01-JUN-2000 Homo sapiens chromosome 8 map 8q24.3-qter clone CTA-393G12, WORKING DRAFT SEQUENCE, 12 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-OCT-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polley,A., Baumgart,C., Blechschmidt,K., Dette,M.D., Jahn,N., Menzel,U., Reichwald,K., Schilhabel,M.B., Schudy,A., Taudien, Wen,G., Siebert,R., Schlegelberger,B. and Rosenthal,A.
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3 (bases 1 to 133075)
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Menzel, U. and Rosenthal, A.
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                                                               1. .133075
                                                                               ocation/Qualifiers
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of 5314
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ORIGIN

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RESULT 13
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                                                                                                                                                         Elhaj.C., Escotto,M., Falls,T., Ferragutto,D., Flagg,M., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Johnson,R., Jolivet,S., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Martinez,E., Massey,E., Maher,G., Miner,G., Miner,G., Metzer,R., Juna,R., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Ngyen,N., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Stantey,H., Shooshtari,N., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Tangan,L.K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
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                                                                                                                          Vera, V., Villalon, D.,
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                                                                                                                                              Vinson, R.,
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On Feb 17, 2001 this sequence version replaced gi:12831332
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is not known and their order in this sequence record is
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Assembly program: Phrap; version 0.990329
Consensus quality: 131116 bases at least Q40
Consensus quality: 134949 bases at least 020
Consensus quality: 136756 bases at least 020
Estimated insert size: 133513; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0x in Q20 bases; agarose-fp estimation
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Center clone name: RP11-8P13B
Center clone name: RP11-8P13B
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SOURCE

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 5, 2000 this sequence version replaced gi:7329377.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Morman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara, V., Raymond,C., Riley,R., Kothman,D.,
Pierre,N., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                 reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Anderson,S., Baldwin,J., Barna,N., Burwan,A., Burkett,G., Castle,A., Boyuslavkiy,L., Boukingalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC019269 152511 bp DNA HTG 05-SEP-2000 Homo sapiens clone RP11-8P13, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                          Sequencing vector: Plasmid; n/a; Sequencing vector: Plasmid; n/a;
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Assembly program: Phrap; version 0.960731
Consensus quality: 148050 bases at least Q40
Consensus quality: 150303 bases at least Q30
                                                                                                                                                                                                               Center clone name: 8_P_13
                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
-------- Project Information
Center project name: L2991
                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                     1.40579710144928Chemistry: Dye-terminator Big
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/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                      ---- Genome Center
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                          96% of reads; %-0.f%% of reads
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence
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                                                                                                                                     Conservative
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/note="assembly_fragment"
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/clone_lib="RPCI-11 Human
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/db_xref="taxon:9606"
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AC037452/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 22, 2000 this sequence version replaced gi:7528181. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarrhy, M., McEran, P., McGurk, A., McKeran, K., McPheeters, R., McCarthy, M., McEran, P., McGurk, A., McKeran, K., McPheeters, R., McCarthy, M., McEran, P., McGurk, A., McKeran, R., Mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J. Tesfaye,S., Theodore,J., Tirell,A., Travers,M., Trigillo,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Connell,P., O'Nell,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. Homo sapiens chromosome 2, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vassiliev, H., Viel, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                      * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* This record will be updated and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, 20 unordered pieces
                                                                                                                                                                                                                                                        Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150666 bases at least Q40
Consensus quality: 156637 bases at least Q30.
Consensus quality: 156637 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 159794; sum-of-contigs
                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 161694)
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                                                                                                                                                                                                           Quality coverage: 4.3 Quality coverage: 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L9452
Center clone name: 650_N_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- Project Information
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clone RP11-650N19 map
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Q20 bases;
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sum-of-contigs
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163: gap of 1
41183: contig of
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14991: contig of 3709 bp
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11182: contig of 2663 bp in length
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contig of 2612
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Human acylcoenzyme Human acyl CoA.cho DNA encoding a pro Human ACAT Related Nucleotide sequenc embB gene probe Mycobacterium tube EST clone Bz28 Cloned bovine herp Bovine herpes viru Lycopene cyclase -	Description

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4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8
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## ALIGNMENTS

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WPI; 1998-032573/03. P-PSDB; AAW43406.	Sturley SL;	(UYCO ) UNIV COLUMBIA NEW YORK.	30-MAY-1996; 96US-0657620.	30-MAY-1997; 97WO-US09460.		04-DEC-1997.	WO9745439-A1.	/*tag= a	CDS 11224	Key Location/Qualifiers		Homo sapiens.		therosclerosis; hyperlipidaemia	este	Acylcoenzyme A:cholesterol acyltransferase II; ARGP-1;		Human acvicoenzyme A:cholesterol acvitransferase II DNA.		08-JUN-1998 (first entry)	AAV01533;	AAV01533 standard; DNA; 1521 BP.	533	ř 1

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AAA88842
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Best Local S
Matches 20
Genetically engineering the biosynthetic pathways in plants involved the accumulation of sterol compounds and tocopherol to produce compounds for lowering the level of low density lipoprotein cholester in blood serum .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This isolated nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase II (see AAW43406), or ACAT related gene product I (ARGP-1), that is expressed at high levels in intestine and is a candidate for sterol esterification in these tissues. It was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see AAV01534) for human ARGP-2 (see AAW43407) was also identified. Also claimed are host vector systems for production of ARGP polypeptides, and transgenic non-human mammals. ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a subject who has an imbalance in sterol levels due to a defect in sterol esterification. A claimed oligonucleotide capable of encorifically bythridisting to a minuma segmence of minipartine in the
                                                                                                                                      WPI; 2000-665136/64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypolipemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyl CoA:cholesterol acyltransferase; ACAT; transgenic plant; sterol; tocopherol; phytosterol; phytostanol; anticholesterolemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human acyl CoA: cholesterol acyltransferase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA88842;
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                                                                                                                                                                                                                   Venkatramesh M,
                                                                                                                                                                                                                                                                            (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000; 2000WO-US09696
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                                                                                                                                                                                                                                                                                                                                   12-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 15A-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid molecule, or a vector expressing the bigonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2 the wild-type enzymes can be used to identify an inhibitor, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically hybridising to a unique sequence of nucleotides in the
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20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tocopherol; phytosterol;
emic; human; ss.
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                                                                                                                                                                                         м, Córbin DR,
Lardizabal KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                99US-0128995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of atherosclerosis or hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 A; 489 C; 412 G;
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Lassner MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                    Boddupalli SS,
W, Rangwala SH,
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                                                                                                                                                                                                                Grebenok RJ;
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밁 δÃ

cholesterol

The present sequence encodes a protein related to acyl-CoA:cholesterol acyltransferase (ACAT) related proteins. ACAT-like proteins are active in the formation of a sterol, ester and/or triacylglycerol from a fatty

Claim 10; Fig 7; 89pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                         Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonar disease or metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sterol brassicastanol. Oil obtained from the seeds can be used in food and pharmaceutical compositions to lower levels of low density lipoprotein cholesterol in blood serum. ACAT enzymes can be used in the present invention to produce elevated levels of phytosterol and/or phytostanol esters.
                                                                                                                                                                                                                                                    05-JUN-1998;
12-NOV-1998;
                                                                                                                                                                                                                                                                                                    04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes; cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity;
                                                                                                                                                                                                                                                                                                                                   09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acyl-CoA:cholesterol acyltransferase; ACAT; ester; triacylglycerol; fatty acyl-CoA; lipi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ45383 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of sterols and tocopherols in transgenic plants. Seeds of such plants may contain elevated levels of sitostanol and/or its esters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholesterol and long chain fatty acids. Recombinant constructs of the invention are used to alter the biosynthesis and accumulation of sterols and tocopherols in transgenic plants. Seeds of such
                                                                                                                                                                                                                      (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                 WO9963096-A2
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a protein related to ACAT-like proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1895 BP; 323 A; 610 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and alpha-tocopherol, and reduced levels of campesterol and campestanol and their esters. The seeds may also contain the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of human acyl CoA:cholesterol acyltransferase (ACAT) full-length DNA. Sterol O-acyltransferases such as ACAT catalyse the formation of cholesterol esters from
                                                                                                                                                                                                                                                                                                                                                                                                                             lipoprotein secretion; adipogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal lipid metabolism; abnormal fat absorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 60-62; 166pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 CTCCCTGCTGGCGCTGATGG 41
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                                                                                                                                                                                       Ruezinsky
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                                                                                                                                                                                                                                                    98US-0088143
98US-0108389
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0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAT-like protein; sterol;
id composition; plant cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1895;
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                                                                                                      cardiopulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC activity, including cancer, diabetes, cardiopulmonary diseases e.g. heart CC activity, and sociated with altered cellular disported with abnormal lipid metabolic disorders, obesity, diseases associated with abnormal lipid metabolicm, and diseases associated with abnormal lipid metabolism, and diseases associated with abnormal lipid metabolism, and diseases associated with abnormal fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                       New nucleic acid encoding a human diacylglycerol acyltransferase, useful for treating hyperlipidemia, atherosclerosis, heart diseas other diseases associated with an imbalance of triglyceride level
                   Claim 4; Fig 1B; 32pp; English.
                                                                                                                                                                   01-OCT-1998;
                                                                                                                                                                                                                                      US6100077-A.
                                                                                                                                                                                                                                                                                                                                                acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
DGAT; cholesterol; triglyceride biosynthesis; hypertriglyceridaemia;
                                                                                                                                                                                                                                                                                                                                                                                                         Human ACAT Related Gene Product 1 ARGP1 coding sequence
                                                                                                                       Sturley SL,
                                                                                                                                                                                         01-OCT-1998;
                                                                                                                                                                                                                08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA76169
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                                                                                        P-PSDB; AAB15200
                                                                                                                                           (UYCO ) UNIV
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              absorption,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 ctccctgctggcgctgatgg 543
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                                                                                                  2000-557622/51.
                                                                                                                                                                                                                                                                                                                                                                                   ACAT Related Gene Product 1; ARGP1; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                       0elkers
                                                                                                                                              COLUMBIA NEW YORK
                                                                                                                                                                    98US-0165042.
                                                                                                                                                                                         98US-0165042
                                                                                                                                                                                                                                                                                Location/Qualifiers 245..1711
                                                                                                                                                                                                                                                           /product= "Human ARGP1"
                                                                                                                                                                                                                                                                                                                                         atherosclerosis;
                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 G;
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                                         imbalance of triglyceride levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 T; 1 other;
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بار 12;
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                                                                                                                                                                                                                                                                                                                                                                                    enzyme;
                                                      disease,
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                                                    or.
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The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates

Query Match

4.88;

Score 16;

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19;

Length 144;

Sequence 144

BP;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeostasis. The present sequence is the coding sequence of human ACAT Related Gene Product 1 (ARGP1). The enzyme encoded by the present sequence is a diacylglycerol acyltransferase (DCAT). ARGP1 does not esterify cholesterol. It is thought therefore that ARCP1 participates in the Coenzyme A-dependent acylation of substrate(s) other than cholesterol e.g. diacylglycerol. Also, ARGP1 has a predicted diacylglycerol binding motif, suggesting that it may perform the last acylation in triglyceride biosynthesis. ARGP1 gene and protein are useful for treating a subject who has an imbalance in triglyceride levels due to a defect in esterification of diglycerol, via gene therapy. Particularly, ARGP1 is useful for treating hypertriglyceridemia, hyperlipidaemia, atherosclerosis, heart disease, obesity or other diseases associated with high or excessive levels of triglyceride.
                                                       This is the nucleotide sequence of a nucleic acid of the human cell line SH-SY5Y, used in the method proteins. The invention involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; SH-SY5Y; apoptosis; antibody; immunohistological staining; inhibition; ds.
                             diseases
                                             the protein, inhibitors.
                                                                                                                                                     Claim
                                                                                                                                                                                  Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis
                                                                                                                                                                                                                                 WPI; 1998-495844/42
                                                                                                                                                                                                                                                                                                                            05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                           05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                         W09839437-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence 3 from human cell line SH-SY5Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV54158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV54158 standard;
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                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sterol esterification, an important component of intracellular lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .823 ctccctgctggcgctgatgg 842
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                                                                                                                                                   1; Page 38;
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It ca
                                                                                                                                                                                                                                                                                               HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                           98WO-JP00905
                                             can
                                                                                                                                                  70pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA;
                                             also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No.
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                                               for
                                             treatment of
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0.12;
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                                           apoptosis-related
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The present invention relates to oligonucleotides based on nucleotide CC sequences obtained from both wild-type tubercle bacilli (wtTB) that are CC susceptible to a drug and mutant-type tubercle bacilli (wtTB) that are CC resistant to a drug and mutant-type tubercle bacilli (mtTB) that are CC rifampicin (RFP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and CC resistance (EB). The rpoB gene is responsible for resistance to RFP; the CC responsible for resistance to SM, the inhA gene is responsible for resistance to INH; the katG gene is responsible for resistance to INH; the katG gene is responsible for resistance to INH; the katG gene is responsible for resistance to INH; the katG gene is responsible for resistance to INH; the satG gene is responsible for for invention also relates to nucleic acid probes having part of a nucleotide confidence of tubercle bacilli (TB) responsible for drug resistance and CC primers used to generate the probes. The present sequence is an occupance of the present invention. The oligonucleotides of the present invention can be used to enable the differentiation of drug cresistance and the determination of infection with tubercle bacilli
                                                          Query Match 4.8
Best Local Similarity 100
Matches 16; Conservative
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                                                                                                                                     Sequence 150 BP;
           125
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 64; 114pp; English.
                25 CCTGCTGGCGCTGATG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle bacilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-246696/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISN ) NISSHINBO IND INC. (SYST-) SYSTEM RES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2000; 2000EP-0306563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tubercle bacillus; drug sensitivity; drug resistance; rifampicin; streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene; rpsL gene; inhA gene; katG gene; embB gene; probe; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1076099-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embB gene probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF95166 standard; DNA; 150 BP.
cctgctggcgctgatg 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 AGATACAGACAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishida M,
                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0220357
                                                                                                                                A; 50 C; 43
                                                                      100.0%;
                                                                                        4.8%;
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                                                   Score 16; DB Pred. No. 21; 0; Mismatches
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                                                                                                                          31 T; 0 other;
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                                                                   DB 22;
21;
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217 cctgctggcgctgatg

CCTGCTGGCGCTGATG 40

Matches Query Match Best Local

Local

l Similarity 16; Conserv

4.8%; 100.0%;

Score 16; DB; Pred. No. 21; 0; Mismatches

DB 21; 21; 0,

Length 300; Indels

0;

Gaps

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Conservative

0;

25

Sequence

300

B₽;

44 A; 101 C;

92 G;

63 T; 0 other;

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The present sequence is that of the Mycobacterium tuberculosis CC embB (ethambutol resistance) gene (bp7741-8040). Amplification CC and cycle sequencing primers (see AAA4983-62) are used for the CC detection and analysis of antibiotic resistance-associated mutations CC PR (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (cc (streptomycin)) and 23S (azithromycin) genes of M. tuberculosis. CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. CC (haracterization of M. tuberculosis present in a sputum sample. CC without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12 cm d. 23S genes for the presence of antibiotic mithousis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the sence of antibiotic resistance-inducing mutations. Genotypic customic contributic resistance-inducing mutations. Genotypic antibiotic resistance-inducing mutations. Genotypic contribiotic resistance-inducing mutations.
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ID AAA4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 8; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-431611/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis embB gene (ethambutol resistance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA49869 standard; DNA; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance; embB gene; ethambutol resistance; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0111794.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
complement(21..41)
/*tag= a
/note= "primer of AAA49847"
280..300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "primer of AAA49848"
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PD ΣX

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AAV89118
ID AAV8
AAX91
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                                                                                           RESULT
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                                                                                                                                                                                       Query Match
Best Local S
Matches 16
                                                                                 1501
                                                                                                                                                                                                                                                                             The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, catholic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
            28-SEP-1999
                                       AAX91501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV89118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV89118 standard;
                                                                  AAX91501 standard;
                                                                                                                                                                                                                                                         Sequence 507 BP; 122 A; 105 C; 101 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Racie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST clone BZ288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-1999
                                                                                                                                   173
                                                                                                                                                            166 AGAATAGTGGGAGTCT 181
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                                                                                           ဖ
                                                                                                                                l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N, Jacobs
Spaulding
                                                                                                                                                                                       Conservative
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97us-0838821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US06955
                                                                                                                                                                                                                                                                                                                                                                                                                                                            618pp; English.
                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         < ~
                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                    4.8%; Score 16; DB
100.0%; Pred. No. 22;
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                                                                  ΒP
                                                                                                                                                                                       0
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                  20;
                                                                                                                                                                                       0
                                                                                                                                                                                                               Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from
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                                                                                                                                                                                       Gaps
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AAX91502
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                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunegens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TMF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence represents a BHV-2 thymidine kinase partial gene sequence, BHV-2UK cloned for use in the invention. This differs from the previously published sequence BHV-2NY-1 by having adenine at position 727 (full length)
                                                                           Bovine herpes virus-2; BHV-2; cytokine; immune response; imminterleukin; colony stimulating factor; CSF; interferon; IFI tumour necrosis factor; recombinant virus; vaccine; mucosal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin; colony stimulating factor; CSF; interferon; IF tumour necrosis factor; recombinant virus; vaccine; mucosal mastitis; breast cancer; stress induced disease; thymidine
                                                             mastitis; breast cancer; stress-induced disease; thymidine kinase;
                                                                                                        Bovine herpes virus-2; BHV-2;
                                                                                                                                          Bovine herpes virus 2 thymidine kinase partial gene sequence
                                                                                                                                                                                                                                            AAX91502 standard; DNA; 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 528 BP; 114 A; 176 C; 151 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides bovine herpes virus-2 (BHV-2) based vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY29085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-255101/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradley AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine herpes virus-2; BHV-2; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloned bovine herpes virus 2 thymidine kinase partial gene sequence
                                                                                                                                                                            28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 4A-C; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         instead of guanine.
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                           24 CCCTGCTGGCGCTGAT 39
                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          herpes virus-2 vectors
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duffas WPH;
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            4.8%;
                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                         DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response; immunogen; IL;
                                                                                          immune response; immunogen; IL;
CSF; interferon; IFN; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        20; Length 528,
                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFN;
                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
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Bovine herpesvirus

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Best Local Similarity
Matches 16; Conserv
 03-AUG-1990;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                             CDS
                                                     04-AUG-1991;
                                                                               05-SEP-1991.
                                                                                                        W09113078-A.
                                                                                                                                                                                                    Erwinia
                                                                                                                                                                                                                           GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss
                                                                                                                                                                                                                                                       Lycopene cyclase - native.
                                                                                                                                                                                                                                                                                   26-NOV-1991
                                                                                                                                                                                                                                                                                                            AAQ13722;
                                                                                                                                                                                                                                                                                                                                    AAQ13722 standard; DNA; 1234 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunogens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence represents the partial sequence of a previously published BHV-2 thymidine kinase, BHV-2NY-1. The cloned BHV-2UK sequence (AAX91501) of the invention differs from the present sequence BHV-2NY-1 by having adenine at position 727 (full length) instead of guanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 559 BP; 123 A; 178 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides bovine herpes virus-2 (BHV-2) based vectors that comprise at least one cytokine-encoding DNA sequence. The expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bovine herpes virus-2 vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-255101/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       241 ccctgctggcgctgat 256
                                                                                                                                                                                                                                                                                                                                                                                                                                24 CCCTGCTGGCGCTGAT 39
                                                                                                                                                                                                   herbicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                (first entry)
90US-0562674.
90WO-4807613.
90US-0525551.
                                                     91WO-US01458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4A-C; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97GB-0020633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-GB02927
                                                                                                                                                                       Location/Qualifiers
                                                                                                                            /*tag= a
/label= lycopene_cyclase
                                                                                                                                                                                                EHO-10 (E. vulneris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 T; 0 other;
                                                                                                                                                                                                  ATCC 39368).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 12
AAQ13723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                              03-AUG-1990;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacterio 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are represented in AAQ13716, AAQ13718, AAQ13719, AAQ13722, AAQ13724 and This native communications.
Ausich RL, Brinkhaus FL,
                                                                                                04-AUG-1991;
                                                                                                                                                                                                CDS
                        (STAD ) AMOCO CORP.
                                                                                                                        05-SEP-1991
                                                                                                                                                WO9113078-A.
                                                                                                                                                                                                                                 Erwinia herbicola EHO-10 (E.
                                                                                                                                                                                                                                                        GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss
                                                                                                                                                                                                                                                                                  Lycopene cyclase - variant
                                                                                                                                                                                                                                                                                                           26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This native sequence was genetically engineered for use expression in yeast, see AAQ13723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ausich RL,
Yen HC;
                                                                                                                                                                                                                                                                                                                                                           AAQ13723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1234 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant expression plasmids can be used of the enzymes and hence large amts. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are a total of six relevant genes in a 7900 bp region that cause E. coli cells to produce GGPP and the carotenoids phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 19(1-3); 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthesis of carotenoid(s) in genetically engineered using DNA encoding enzymes from Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                             125 TCTATCAGCTCACCCG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-281410/38
                                                                                                                                                                                                                                                                                                                                                                                                                    896 tctatcagctcacccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brinkhaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
                                              90US-0562674.
90WO-4807613.
90US-0525551.
                                                                                                91WO-US01458
                                                                                                                                                                      /label= lycopene_cyclase
                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                19..1140
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                      911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
Mukharji I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mukharji I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                  vulneris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ç;
                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 T;
Proffitt JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
22;
                                                                                                                                                                                                                                  ATCC 39368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proffitt JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to produce large amts. carotenoids which they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Yarger JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yarger JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Ma
Best Loc
Matches
30-OCT-1991;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are a total of six relevant genes in a 7900 bp region that cause E. coll cells to produce GGPP and the carotenoids phytoene through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 158:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase 4H, lycopene cyclase, beta carotene hydroxylase, and zeaxanthin glycosylase are represented in ANQ13716, ANQ13718, ANQ13719, ANQ13722, ANQ13724 and ANQ13726 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The native sequence (AAQ13722) was genetically engineered for use expression in yeast. At the 5' end of the gene, the native initiation GTG codon has been an ATG codon. The second amino acid residue, Arg, was originally encoded by an AGG codon that was changed to a CGG codon, while retaining its coding for the Arg amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant expression plasmids can be used of the enzymes and hence large amts. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis of carotenoid(s) in genetically engineered hosts using DNA encoding enzymes from Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yen
                                                                                                        US5530188-A
                                                                                                                                                                                                   Erwinia herbicola
                                                                                                                                                                                                                                                                  GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene;
                                                                                                                                                                                                                                                                                              Lycopene cyclase
                                                                                                                                                                                                                                                                                                                        11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                             AAT40795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1234
                                                     02-MAR-1990;
                                                                              25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             896 tctatcagctcacccg 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TCTATCAGCTCACCCG 140
                                                                                                                                                                                                                                       lgment; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1991-281410/38
DB; AAR13987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
16; Conserv
                                                                                                                                                                                                                            ribulose
                                                                                                                                                                                                                           dehydrogenase-4H; carotenoid; C4O; zeaxanthin; diglucoside; food colourant; chloroplast transit peptide; increase yield; ribulose bis-phosphate carboxylase-oxygenase; ss.
                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 19(1-3);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
91US-0785566.
90US-0487613.
90US-0525551.
                                                     90US-0487613
                                                                                                                                           /*tag=
                                                                                                                                /product= lycopene_cyclase
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                              coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                            DNA; 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to produce large carotenoids which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
AAT40796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1990;
28-FEB-1991;
21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manipulation of the present sequence, the lycopene cyclase coding sequence, by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. Other enzymes involved in the carotenoid biosynthesis pathway include geranylgeranyl pyrophosphate (AAW01113), phytoene synthase (W01121) and phytoene dehydrogenase-4H (AAW01123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing prodm. of total carotenoid(s) in a higher plant - transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ausich
Yarger
                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotene(24); zeaxanthin; diglucosid pigment; food colourant; chloroplast transit peptide; increase yie tobacco ribulose bis-phosphate carboxylase-oxygenase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT40796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT40796 standard; DNA; 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1235 BP; 202 A; 384 C; 405 G; 244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 17; Column
                                                                                                                                                                                                                                                                                                                                                                                   Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TCTATCAGCTCACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 897 tctatcagctcacccg 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lycopene cyclase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brinkhaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0562674.
91US-0662921.
93US-0095726.
                                                                                                                                                                                                                  /*tag= a
/product=
18..1165
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99-102; 99pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FL,
                                                                                                                                                             "SphI-BamHI fragment;
                                                                                                                                                                                                                                            lycopene_cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mukharji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diglucoside;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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02-MAR-1990; 25-JUN-1996

90US-0487613

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RESULT 15
AAT91547
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밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1990;
28-FEB-1991;
21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1991;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ausich RL,
Yarger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a recombinant lycopene cyclase coding sequence. The approx. 1142 bp SphI-BamHI fragment present in the plasmid pARC1509 (ATCC 40850) is used to transform plants in order to increase the level of carotenoids produced by plants. Manipulation of it by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and beta-carotene is an effective and apparently harmless food colourant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. Other enzymes involved in the carotenoid biosynthesis pathway include geranylgeranyl pyrophosphate (AAW01119), phytoene synthase (WO1121) and phytoene dehydrogenase-4H (AAW01123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Fig 19; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW01125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STAD ) AMOCO CORP.
                                                                                                                                                       Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP; lycopene cyclase; recombinant enzyme; transgenic organism;
                                                                                                                                                                                                                              15-JAN-1998
                                                                                                                                                                                                                                                        AAT91547;
                                                                                                                                                                                                                                                                                    AAT91547 standard; DNA; 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1235 BP; 198 A; 388 C;
                                                                                                                                                                                                 Erwinia herbicola lycopene cyclase structural gene
                                                                                                                                                                                                                                                                                                                                                      US5656472-A.
                                                                                                              Erwinia herbicola.
                                                                                                                                           beta-carotene; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996-308823/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brinkhaus
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-0785566.
90US-0487613.
90US-0525551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-0562674.
91US-0662921.
93US-0095726.
                          /*tag= a
/product= Lycopene_cyclase
/transl_except= (pos:20..22,aa:Met)
                                                                    Location/Qualifiers 20..1144
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FL,
                                                                                                                                           plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mukharji I,
                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16;
Pred. No.
                                                                                                                                              vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 G;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                              A; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proffitt
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 1235; 22;
                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                               SS
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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0;

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Search completed: August 24, 2001, 04:36:49 Job time: 2584 sec
                                                              В
                                                                                   QΥ
                                                                                                                          Query Match
Best Local
                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1990;
03-AUG-1990;
28-FEB-1991;
07-JUN-1995;
                                                                                                                                                                                               A novel DNA molecule has been isolated which encodes an Erwinia herbicola lycopene cyclase enzyme that converts lycopene to beta-carottene? The DNA molecule comprises at least 1125 bp and is present in the plasmids pARC147, pARC1509, pARC1510 and pARC1520. The present sequence represents the structural gene for lycopene cyclase. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yearsts or plants, with increased beta-carotene levels. Beta-carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-414592/38.
P-PSDB; AAW32474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                 DNA encoding Erwinia herbicola lycopene cyclase – for produrecombinant-enzyme, and transgenic organisms with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                            Yarger
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ausich
                                                                                                                                                                                                                                                                                                                             Example 17;
                                                                                                                                                                                                                                                                                                                                                     beta-carotene levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STAD ) AMOCO CORP.
                                                                                                                                                                         Sequence 1235 BP; 202 A; 384 C;
                                                              897 tctatcagctcacccg 912
                                                                                      125 TCTATCAGCTCACCCG
                                                                                                                        Local.
                                                                                                                                                                                                                                                                                                                                                                                                                                           RL,
J,
                                                                                                            l Similarity
                                                                                                                                                                                                                                                                                                                              Fig 19; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brinkhaus
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0095726.
90US-0487613.
90US-052551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-0562674
91US-0662921
                                                                                                                            4.8%;
100.0%;
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Pred. No.
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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US-08-812-203-4
US-09-300-864-4
US-09-300-864-4
US-09-300-864-3
US-08-442-248-3
US-08-442-248-3
US-08-440-815-3
US-08-803-972-6
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US-08-803-972-11
US-08-803-972-1
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ior ior intt, itt, is:	tch al Similarity 100.0 al Similarity 100.0 20; Conservative CTCCCTGCTGCTGCTGATGG	42-2 2, Application US/09165042 NFORMATION: T: Sturley, Stephen L. T: Oelkers, Peter TINVENTION: ACYLTRANSFERAS ERENCE: 0575/56331 APPLICATION NUMBER: US/09/ FILING DATE: 1998-10-01 FIED ID NOS: 32 PATENTION PROS: 32 PATEN		3697 3697 3697 4371 43795 37 37 39 39 39 39 39 39 39 39 39 39 39 39 39
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ssis in Hosts sing Dept	8; Length 1976; 8) 0; Indels 0;	NG DIACYLGLYCEROL		Sequence
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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; MOLECULE TYPE:
US-08-095-726-13
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
            ATTORNEY/AGENT INFORMATION:
                                                           PRIOR APPLICATION DATA:
                                                                                                              SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,72
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
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LENGTH: 1235 base pairs
TYPE: nucleic acid
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                                                                                FILING DATE: 21-JUL-1993 CLASSIFICATION: 435
                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100 nes 16; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                               APPLICATION NUMBER: US 07/785,566
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                                                                                                                                                                                                                                                                                      Chicago
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                                                                                                                                                                                                                                                                                                        200 E Randolph St
                                                                                                                                                                                                                                                       USA
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Mukharji, Indrani
Proffitt, John H
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No. 5530188val B
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Best Local
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
                                                                                                                                                                                                                        FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
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LENGTH: 1235 base pairs
TYPE: nucleic acid
REFERENCE/DOCKET NUMBER: AM TELECOMMUNICATION INFORMATION:
                                                                                                                     FILING DATE: 18-MAY-1990 PRIOR APPLICATION DATA:
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                 FILING DATE: 02-MAR-1990 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: U
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APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Blosynt
TITLE OF INVENTION: Glycosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                        APPLICATION NUMBER: US 07/562,674 FILING DATE: 03-AUG-1990
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 120 S. CITY: Chicago
                                 REGISTRATION NUMBER: 29,381
                                                                                                       APPLICATION NUMBER:
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                                                 Gamson, Edward P
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120 S. Riverside Plaza, 22nd Floor
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3128564972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biosynthesis of Zeaxanthin and Glycosylated Zeaxanthin in Genetically Engineered Hosts
                                                                                                                                                       US 07/525,551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 07/662,921
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/805,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
POSITION IN GENOME:
MAP POSITION: -1
                                                                                                   APPLICATION NUMBER: FILING DATE: 18-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BITITLE OF INVENTION: GINUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                              APPLICATION NUMBER: US 07/487,613 FILING DATE: 02-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                NAME: Gamson, Edward P. REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 09-DEC-1991
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01 FILING DATE: 22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
REFERENCE/DOCKET NUMBER: AMO-006.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Welsh & Katz, Ltd.
120 S. Riverside Plaza, 22nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brinkhaus, Friedhelm L.
Mukharji, Indrani
Proffitt, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yarger, James G.
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                                                                                                               UMBER: US 07/525,551
18-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blosynthesis of Zeaxanthin and Glycosylated Zeaxanthin in Genetically Engineered: 104
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                                                                                                                                                                                                                                                                                                                                                                 US/08/096,623A
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Pred. No.
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                                                                            ; NAME/KEY:
; LOCATION:
US-08-259-264-1
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                                                                                                                                                                                                                            TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: pp60PIK: A DOWNSTREAM ELEMENT IN INSULIN SIGNALING NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MAP POSITION: -1
UNITS: bp
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 5737 base pairs
                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                      MOLECULE TYPE:
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                                                                                                                        FEATURE:
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TYPE: n
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                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: linear
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                                                                                                                                                                STRANDEDNESS:
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DEDNESS: single
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                                                                                                                                                                                nucleic acid
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N: 435
                                                                                                                                                                single
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100.08; ...
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tive 0;
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                                Length 5737;
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US-08-822-586-45
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Sequence 45, App-
Sequence 45, App-
No. 6015890
                                                                                                                                                                                                               Sequence 3, Application US/08203806B Patent No. 5714575
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/822
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 9670
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10507-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                    7803 CCTGCTGGCGCTGATG 7818
                                                                                     APPLICANT:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
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                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      25 CCTGCTGGCGCTGATG 40
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ZIP: 10016
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 ADDRESSEE:
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                                 LE OF INVENTION: Nucleic Acid Sequences, Stress-induced LE OF INVENTION: Proteins and Uses Thereof BER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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Y: U.S.A.
                                                                                 : Jones, Pamela
Etchegaray, Jean-Pierre
Weining, Jian
Pollitt, N. Stephen
Goldstein, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
Weiser & Associates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 16; DB 3; 100.0%; Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-875-8383
TELEPACE: 215-875-8394
TELEX: 834809 WEISTAK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/203,806B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5998P
TELECOMMUNICATION 1975-8383
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09106217 Patent No. 6063576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 CTGCATGAGGCACCA 608
                                                                                                                                                                                                                                                        STREET: 555 Thirteenth
STREET: Tower
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 15; Conserv
                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 CTGCATGAGGCACCA 113
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                       APPLICATION NUMBER: US/09/106,217
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                                                                                                                                                                                                                                             STATE:
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686..895
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                                                                                                                                                                                                                                                                                                                                                                     Cardiomyopathy, a Heritable Form of Heart Failure
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                   Ernst & Kurz, P.C.
et, N.W., Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:

38,609

2323-125

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 1, Application US/09106217 atent No. 6063576 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE NU HYPOTHETICAL: NU
                                                                                          TELEFAX: 202-783-6031
NFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                  APPLICATION NUMBER: US/09/106,217
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1134 base pair
                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-783-6040
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              TOPOLOGY:
                           STRANDEDNESS:
                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                      TELEPHONE:
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                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           5: Rothwell, Figg, Ernst & Kurz, P.C.
555 Thirteenth Street, N.W., Suite 701 East
                                                         1134 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-783-6031
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; Pred. No.
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Query Match
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; LOCATION:
US-09-106-217-1
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                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,084
FILING DATE: 30-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/690,840
FILING DATE: 23-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,293
FILING DATE: 14-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                          STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: FEATURE:
                                                                                                                                                      REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                    FILING DATE: 14-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two ..... CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
NAME/KEY: CDS
                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                        nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%;
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; LOCATION: 1..1350
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-462-351-1
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5468481-2/c
;Patent No. 5468481
; APPLICANT: SHARMA,
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5194425-2/c
                                                                                   5194425-2
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Best Local S
Matches 15
                                                                                                            FILING DATE:
SEQ ID NO:2:
                                                                                                                                                                                                      TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL AMELICATING AUTOIMMUNITY NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                BRIAN R.
                                                                                                                                                                                                                                                                                              Patent No.
Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                             APPLICATION NUMBER: US/07/
FILING DATE: 21-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L. TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            APPLICANT: SHARMA , SOMESH D.; LERCH, L. BERNARD; CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-APR-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 690,840
FILING DATE: 23-APR-1991
APPLICATION NUMBER: 576,084
FILING DATE: 30-AUG-1990
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
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les 15; Conserv
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nes 15; Conservative
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                                                                                                 LENGTH: 1356
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         4.5%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
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100.0%; Pred. No.
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alpha subunit"
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16;
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US-08-812-203-4
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                                                                                                                                                           RESULT 15
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Patent No. 5958
                                                                                                            Sequence 4, Application US/09300864 Patent No. 6214972
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: WALLEN III, JOHN W:
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                             GENERAL INFORMATION: APPLICANT: ABRAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/812,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                             1145 CTGCTGGCGCTGATG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AGACAGCAAAACGGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                                                                                                         26 CTGCTGGCGCTGATG 40
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METTERS, KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABRAMOVITZ, MARK
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SAWYER, NICOLE
METTERS, KATHLEEN
SLIPETZ, DEBORAH
VENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
                                                                ABRAMOVITZ, MARK BOIE, YVES
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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100.0%;
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DNA ENCODING PROSTAGLANDIN RECEPTOR DP
                                                                                                                                                                                                                                                                                            Score 15; DB; Pred. No. 17;
                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                             Mismatches
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0

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CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE; JOHN W. WALLEN, III
STREET; 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
STATE: NJ
COUNTRY: USA
ZIP: 07055-0900
COMPUTER RENDABLE FORM:
MEDIUM TYPE: PLOPPY disk
COUNTRY: WSA
COUNTRY: WSA
COUNTRY: WSA
COUNTRY: WSA
COUNTRY: PC-DSS/MS-DOS
COMPUTER: IN FC-COMPAILED
PRANTING SYSTEE: PC-DSS/MS-DOS
COMPUTER: USA
SOSTWARE: DRECHGIT RELEASE #1.0, Version #1.25
COUNTRY: APPLICATION BATA:
APPLICATION MUMBER: US/09/300,864
FILING DATE:
APPLICATION MUMBER: US/09/300,864
FILING DATE:
APPLICATION MUMBER: US/09/300,864
FILING DATE:
APPLICATION NUMBER: US/09/300,864
FILING DATE:
APPLICATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 35,403
REFER
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em\_esthum24:\*
em\_esthum25:\*
em\_esthum26:\*

em\_esthum22:\*
em\_esthum23:\*

em\_esthum20:\*
em\_esthum21:\*

em\_esthum16:\*
em\_esthum17:\*
em\_esthum18:\*
em\_esthum19:\*

em\_esthum27:\*
em\_esthum28:\*
em\_estin1:\*
em\_estin2:\*
em\_estin4:\*
em\_estin4:\*
em\_estin5:\*

em\_estom2:

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Gapop 60.0 , Gapext 60.0
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336
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est7:*
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gb_est5:*
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gb_est11:*
gb_est12:*
gb_est13:*
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em\_estpl6: em\_estpl7:

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em\_estov2:\*
em\_estp11:\*
em\_estp12:\*
em\_estp13:\*
em\_estp14:\*

em\_estro15:\*
em\_estro16:\*
em\_estro17:\*
em\_estro18:\*

em\_estrol1:\*
em\_estrol2:\*

em\_estrol0:\*

em\_estro13:\*
em\_estro14:\*

em\_estro4:\*
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em\_estro19:\*
em\_estro20:\*
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gb\_est44:\* gb\_est45:\*

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9b_est110:
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9b_tc:*
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em_gss_humd:*
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em_gss_rod6:*
em_gss_liv4:*
em_gss_liv
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Pred. No. is the number of results predicted by chance to have a and is derived by analysis of the total score distribution

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em\_estro23:\*
em\_htc:\*
gb\_est107:\*
gb\_est108:\*
gb\_est109:\*

Result No.

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RESULT 1
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AV607888
3', mRNA
AV607888
                                                                       cow.
Bos taurus
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bosinae; Bos 1 to 509)
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Match
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                                                                                                                                                                                                ALIGNMENTS
                      Takasuga,A.,
                     Itoh, R., Jitohzono, A. and
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AA4173800 Ze99f02.r
AA117380 Ze99f02.r
BF844007 MR2-HT104
BF733499 RC6-AN006
AZ015284 RPC1-23-2
AW964683 EST376756
BE337999 601290548
AQ984383 RPC1-23-3
BF995676 MR2-GN012
BE337441 601289079
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BF400681 UI-R-CA0-
BF394149 UI-R-CA0-
BE032856 132939 MA
BG293757 602390647
AU135898 AU135898
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AQ835617 HS_5324_A
AQ835618 HS_5051_B
B92301 CIT-HSP-217
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AZ252159 RPCI-23-9
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AL557241
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VERSION
KEYWORDS
SOURCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                 FEATURES
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                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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5', mRNA sec
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                      Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing.
This clone was obtained from Location/Qualifiers
                                                                                                              Single pass sequencing.
This clone was obtained from Location/Qualifiers
                                                                                                                                                                                                         bovine cDNA sequencing
Unpublished (2000)
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.

1 (bases 1 to 539)
Sugimoto,Y., Hirotsune,S.,
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                         Suzuki, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                              Email: kazusugi@cocoa.ocn.ne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125
  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DHIOB"
/note="Vector: pZLI; Site_1: Sal1; Sit
was deleted from a Not1 site"
a 116 c 157 g 110 t 1 oth
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sequence.
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly
was deleted from a Not1 site"
133 c 123 g 126 t
                              /clone_lib="Bos taurus brain fetus"
/tissue_pe="burain"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1BR036H10"
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brain fetus
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Gaps

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Bovoidea;

REFERENCE

TITLE AUTHORS KEYWORDS VERSION ACCESSION O O

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RESULT
AV663814
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                                                                                           RESULT 4
AV663492/c
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Best Local S
                     KEYWORDS
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Best Local Similarity
Matches 26; Conserv
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1 AV663814 Bos taurus bra.
5', mRNA sequence.
AV663814 1 GI:9922844
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                         AV663492
AV663492
3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine cDNA sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: kazusugi@cocoa.ocn.ne.jp
                     EST.
                                 3', mRNA sequence.
AV663492
AV663492.1 GI:992
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Bos taurus brain fe
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/clone="E1BR038G07"
/clone=1ib="Bos taurus brain fetus"
/tissue_type="brain"
/dev_stage="fetus"
                                                                      409 bp mRNA
Bos taurus brain fe
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                 /note="Vector: pZL1; Site_1: Sal1; was deleted from a Not1 site" 144 c 129 g 128 t
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                   GI:9922522
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Bos taurus
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thes 0;
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cDNA clone E1BR036H10
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Best Local :
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                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bovine cDNA sequencing
Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
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AV663813.1
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AV663813
3', mRNA
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This clone was obtained from a polyA-deleted
Location/Qualiflers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                       EST.
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                                                                                                                   Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishisigo, Nishi-shirakawa, Fuki
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Rum
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                          COW.
                                                                                                                                                                                                  Unpublished (2000)
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                               Suzuki,H.
                                                                                                                                                                                                                                                         Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                                                        Bos taurus
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                                                                           Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library
                                                                                                                                                                                                                                 bovine cDNA sequencing
                                                                                                        Email: kazusugi@cocoa.ocn.ne.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElBR036H10"
/clone="b="Bos taurus b.
/tissue_type="brain"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was
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/note="Vector: pZL1; Site_1: ',
/note="Vector: pZL1; Site_1: ',
/note "Vector: pZL1; Site_1: ',
/note "DH10B" a Not1 site"
was deleted from a Not1 site"
was deleted from a Not1 site"
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1BR038G07"
                                                1. .414
                                                          Location/Qualifiers
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Ruminantia; Per
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 409;
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cDNA clone E1BR038G07
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                                                                                                                                                                                                                                                                                                                  ta; Euteleostomi;
Pecora; Bovoidea
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RESULT 6
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Best Local
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BE121364 BE121364 .1 GI:8513469 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 435)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
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                                                                                                 /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
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/clone="Ib="UI-R-CAO"
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/note="vector: pT713D-Pac (Pharmacia) with a modified
/note="vector: pT713D-Pac (Pharmacia) with a modified
/note="vector: pt713D-Pac (Interpretation of the following
/note="vector: pt713D-Pac (Interpretation of the following
/note="vector: pt713D-Pac (Interpretation of the following
/note="vector: pt13D-Pac (Interpretation of the following
/tissues: thalamus, cerebellum, hypothalamus, medulla, pons
/midbrain, cerebral cortex, corpus striatum, testis, and
/nipocampus, For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.ulowa.edu. The subtraction has been
                       Q
                site at ratest.eng.uiowa.edu. Ti
previously described in (Bonaldo,
Genome Research 6:791-806, 1996)
TAG_SEC-None found"
a 106 c 114 g 115 t
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/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: p2L1; Site_1: Sal1; Site_2: Not1; Poly A was deleted from a Not1 site"; 112 c 133 g 82 t
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Pred. No.
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0.019;
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                                                                                       Lennon and Soares,
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF400681 437 bp mRNA EST 28-UI-R-CAO-bhe-c-02-0-UI.S1 UI-R-CAO Rattus norvegicus UI-R-CAO-bhe-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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Bonaldo, M.F., Lennon
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//note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
                                                                                                                                                                                   TAG_SEQ=None found"
106 c 114 g
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previously described in (Bonaldo,
Genome Research 6:791-806, 1996)
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/clone_lib="UI-R-CAO"
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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451 Eckstein Medical Research Building Iowa City,
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Program for Rat Gene Discovery and Mapping
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//lab_host="PHIOB (Life Technologies)"
//note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at tract cor unous con "The mintraction has been site at tract cor unous con "The mintraction has been site of the library control of the library from which this clone was derived, please visit our web site at tract cor unous con "The mintraction has been site of the library control of the library cont
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/db_xref="taxon:10116"
/clone="UI-R-CA0-bha-c-12-0-UI"
/clone_lib="UI-R-CA0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 711) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Keele, J.W.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10371 row: n column: 12
                                                                                                                      Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies,
                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence
BG293757
                                                                                                                                                                                                                                                                                                                                                                                                                       602390647F1 NIH_MGC_94 Mus
                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                 house mouse
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178 c 149 g 110 t
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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0.019;
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clone IMAGE:4502603 5',
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11 TTTTCTATGCTCTCCCTGCTGG 32
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AU135898
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                           Similarity 100 22; Conservative
                                                                                                                                                                                                                                             Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                         Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                   Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                             HRI human cDNA project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NH_MGC_94"
/tissue_type="retina"
/lab_host="NH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 196 c 150 g 185 t
                                                                                                                  /tissue_type="placenta"
/note="Vector: pME18SFL3"
207 c 197 g 180
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1003129"
/clone_lib="PLACE1"
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                                         DB 108;
0.078;
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PLACE1003129 5', mRNA
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                         Li.W.B., Gruber.C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                  Mammalia; Eutheria;
1 (bases_1 to 952)
                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                     AL537924 952 bp mRNA EST 13-FEB-2001
AL537924 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF028Y018 5
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AL541183
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                                                                                                                                                                                                                                                                                                             323
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Pred. No.
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Mismatches

0

0

Gaps

0;

DB 106; 0.079;

Length 900; Indels

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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343
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Full-length cDNA libraries and normalization Unpublished (2001)
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1 (bases 1 to 900)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91006 EVRY cedex - France segref@genoscope.cns.fr,
                                                                         /note-*Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
http://fulllength.invitrogen.com"
238 c 213 g 222 t
                                           fliang@lifetech.com URL :
                                                                                                                                                                                                                                                                                                                      /clone="CSODE005YD14"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                       Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fundner, R.A., Bult C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J. Fine, L.D., Fitzgerald C.I., First, C.J., Fitzgerald C.J., Fine, L.D., Fitzgerald G.J., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Kelley, J.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Shirley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon M.R.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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EST26541 Cerebellum II Homo
AA323481
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                             Venter,J.C.
                                                                                            The Institute for Genomic
                                                                                                                   Bioinformatics
                                                                                                                                                                  96026280
Email: arkerlav@tigr.org
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                                               2 Medical Center
1: 3018699056
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pcMvsporr 6 vector. Library was constructed by Life pcMvsporr 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL: fliangelifetech.com URL: http://fulllength.invitrogen.com" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer five prime end enriched, double-stranded cDNA was digested with Not I and Eco RV sites of the and cloned into the Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA478000 371 bp mRNA EST zu34h07.rl Soares ovary tumor NbHOT Homo sapiens IMAGE:739933 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                         Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA478000
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                            White, Y., Wylie, T., Watersto
WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone_lib="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: brain; Vector: pBluescript SK-; Site_1:
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/db_xref="ATCC (inhost):124262"
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/clone="InAGE:739933"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:2206634
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the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo." 81 t

BASE COUNT ORIGIN

Query Match 6.0%; Score 20; DB 8; Length 371; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 20; Conservative 0; Mismatches 0; Indels

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